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(54) Title: PLANT DEVELOPMENTAL GENES

(57) Abstract: Recombinant polynucleotides and methods for modifying the phenotype of a plant are provided. In particular, the phenotype that is being modified is a plant's structure and development characteristics.

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PLANT DEVELOPMENTAL GENES

RELATED APPLICATION INFORMATION

The present invention claims the benefit from US Provisional Patent Application Serial
5 Nos. 60/166,228 filed November 17, 1999 and 60/197,899 filed April 17, 2000 and "Plant Trait
Modification III" filed August 22, 2000.

FIELD OF THE INVENTION

This invention relates to the field of plant biology. More particularly, the present
invention pertains to compositions and methods for phenotypically modifying a plant.

10

BACKGROUND OF THE INVENTION

Transcription factors can modulate gene expression, either increasing or
decreasing (inducing or repressing) the rate of transcription. This modulation results in
differential levels of gene expression at various developmental stages, in different tissues and cell
types, and in response to different exogenous (e.g., environmental) and endogenous stimuli
15 throughout the life cycle of the organism.

Because transcription factors are key controlling elements of biological
pathways, altering the expression levels of one or more transcription factors can change entire
biological pathways in an organism. For example, manipulation of the levels of selected
transcription factors may result in increased expression of economically useful proteins or
20 metabolic chemicals in plants or to improve other agriculturally relevant characteristics.
Conversely, blocked or reduced expression of a transcription factor may reduce biosynthesis of
unwanted compounds or remove an undesirable trait. Therefore, manipulating transcription
factor levels in a plant offers tremendous potential in agricultural biotechnology for modifying a
plant's traits.

25

The present invention provides novel transcription factors useful for modifying a
plant's phenotype in desirable ways, such as modifying a plant's structure or development.

SUMMARY OF THE INVENTION

In a first aspect, the invention relates to a recombinant polynucleotide comprising
a nucleotide sequence selected from the group consisting of: (a) a nucleotide sequence encoding a
30 polypeptide comprising a sequence selected from SEQ ID Nos. 2N, where N=1-23, or a
complementary nucleotide sequence thereof; (b) a nucleotide sequence encoding a polypeptide
comprising a conservatively substituted variant of a polypeptide of (a); (c) a nucleotide sequence
comprising a sequence selected from those of SEQ ID Nos. 2N-1, where N=1-23, or a

complementary nucleotide sequence thereof; (d) a nucleotide sequence comprising silent substitutions in a nucleotide sequence of (c); (e) a nucleotide sequence which hybridizes under stringent conditions over substantially the entire length of a nucleotide sequence of one or more of: (a), (b), (c), or (d); (f) a nucleotide sequence comprising at least 15 consecutive nucleotides of a sequence of any of (a)-(e); (g) a nucleotide sequence comprising a subsequence or fragment of any of (a)-(f), which subsequence or fragment encodes a polypeptide having a biological activity that modifies a plant's structure and development characteristics; (h) a nucleotide sequence having at least 31% sequence identity to a nucleotide sequence of any of (a)-(g); (i) a nucleotide sequence having at least 60% identity sequence identity to a nucleotide sequence of any of (a)-(g); (j) a nucleotide sequence which encodes a polypeptide having at least 31% identity sequence identity to a polypeptide of SEQ ID Nos. 2N, where N=1-23; (k) a nucleotide sequence which encodes a polypeptide having at least 60% identity sequence identity to a polypeptide of SEQ ID Nos. 2N, where N=1-23; and (l) a nucleotide sequence which encodes a conserved domain of a polypeptide having at least 65% sequence identity to a conserved domain of a polypeptide of SEQ ID Nos. 2N, where N=1-23. The recombinant polynucleotide may further comprise a constitutive, inducible, or tissue-active promoter operably linked to the nucleotide sequence. The invention also relates to compositions comprising at least two of the above described polynucleotides.

In a second aspect, the invention is an isolated or recombinant polypeptide comprising a subsequence of at least about 15 contiguous amino acids encoded by the recombinant or isolated polynucleotide described above.

In another aspect, the invention is a transgenic plant comprising one or more of the above described recombinant polynucleotides. In yet another aspect, the invention is a plant with altered expression levels of a polynucleotide described above or a plant with altered expression or activity levels of an above described polypeptide. Further, the invention is a plant lacking a nucleotide sequence encoding a polypeptide described above. The plant may be a soybean, wheat, corn, potato, cotton, rice, oilseed rape, sunflower, alfalfa, sugarcane, turf, banana, blackberry, blueberry, strawberry, raspberry, cantaloupe, carrot, cauliflower, coffee, cucumber, eggplant, grapes, honeydew, lettuce, mango, melon, onion, papaya, peas, peppers, pineapple, spinach, squash, sweet corn, tobacco, tomato, watermelon, rosaceous fruits, or vegetable brassicas plant.

In a further aspect, the invention relates to a cloning or expression vector comprising the isolated or recombinant polynucleotide described above or cells comprising the cloning or expression vector.

In yet a further aspect, the invention relates to a composition produced by incubating a polynucleotide of the invention with a nuclease, a restriction enzyme, a polymerase; a polymerase and a primer; a cloning vector, or with a cell.

Furthermore, the invention relates to a method for producing a plant having
5 modified structure and development traits. The method comprises altering the expression of an isolated or recombinant polynucleotide of the invention or altering the expression or activity of a polypeptide of the invention in a plant to produce a modified plant, and selecting the modified plant for modified structure and development traits.

In another aspect, the invention relates to a method of identifying a factor that is
10 modulated by or interacts with a polypeptide encoded by a polynucleotide of the invention. The method comprises expressing a polypeptide encoded by the polynucleotide in a plant; and identifying at least one factor that is modulated by or interacts with the polypeptide. In one embodiment the method for identifying modulating or interacting factors is by detecting binding by the polypeptide to a promoter sequence, or by detecting interactions between an additional
15 protein and the polypeptide in a yeast two hybrid system, or by detecting expression of a factor by hybridization to a microarray, subtractive hybridization or differential display.

In yet another aspect, the invention is a method of identifying a molecule that modulates activity or expression of a polynucleotide or polypeptide of interest. The method comprises placing the molecule in contact with a plant comprising the polynucleotide or
20 polypeptide encoded by the polynucleotide of the invention and monitoring one or more of the expression level of the polynucleotide in the plant, the expression level of the polypeptide in the plant, and modulation of an activity of the polypeptide in the plant.

In yet another aspect, the invention relates to an integrated system, computer or
computer readable medium comprising one or more character strings corresponding to a
25 polynucleotide of the invention, or to a polypeptide encoded by the polynucleotide. The integrated system, computer or computer readable medium may comprise a link between one or more sequence strings to a modified plant structure and development trait.

In yet another aspect, the invention is a method for identifying a sequence similar or homologous to one or more polynucleotides of the invention, or one or more polypeptides
30 encoded by the polynucleotides. The method comprises providing a sequence database; and, querying the sequence database with one or more target sequences corresponding to the one or more polynucleotides or to the one or more polypeptides to identify one or more sequence members of the database that display sequence similarity or homology to one or more of the one or more target sequences.

The method may further comprise of linking the one or more of the polynucleotides of the invention, or encoded polypeptides, to a modified plant structure and development characteristics phenotype.

BRIEF DESCRIPTION OF THE DRAWINGS

5 Figure 1 provides a table of exemplary polynucleotide and polypeptide sequences of the invention. The table includes from left to right for each sequence: the SEQ ID No., the internal code reference number (GID), whether the sequence is a polynucleotide or polypeptide sequence, and identification of any conserved domains for the polypeptide sequences.

10 Figure 2 provides a table of exemplary sequences that are homologous to other sequences provided in the Sequence Listing and that are derived from *Arabidopsis thaliana*. The table includes from left to right: the SEQ ID No., the internal code reference number (GID), identification of the homologous sequence, whether the sequence is a polynucleotide or polypeptide sequence, and identification of any conserved domains for the polypeptide sequences.

15 Figure 3 provides a table of exemplary sequences that are homologous to the sequences provided in Figures 1 and 2 and that are derived from plants other than *Arabidopsis thaliana*. The table includes from left to right: the SEQ ID No., the internal code reference number (GID), the unique GenBank sequence ID No. (NID), the probability that the comparison was generated by chance (P-value), and the species from which the homologous gene was identified.

20

DETAILED DESCRIPTION

The present invention relates to polynucleotides and polypeptides, e.g. for modifying phenotypes of plants.

25 In particular, the polynucleotides or polypeptides are useful for modifying traits associated with a plant's structure or development characteristics when the expression levels of the polynucleotides or expression levels or activity levels of the polypeptides are altered. Specifically, the polynucleotides and polypeptides are useful for modifying the structure and size of flowers, leaves, roots, the plant as a whole, or the like, apical dominance, branching patterns, number of organs, organ identity, whether a plant is sterile or not, the vascularization of a plant, 30 or the developmental staging of a plant, such as when senescence is triggered.

The polynucleotides of the invention encode plant transcription factors. The plant transcription factors are derived, e.g., from *Arabidopsis thaliana* and can belong, e.g., to one or more of the following transcription factor families: the AP2 (APETALA2) domain transcription

factor family (Riechmann and Meyerowitz (1998) J. Biol. Chem. 379:633-646); the MYB transcription factor family (Martin and Paz-Ares (1997) Trends Genet. 13:67-73); the MADS domain transcription factor family (Riechmann and Meyerowitz (1997) J. Biol. Chem. 378:1079-1101); the WRKY protein family (Ishiguro and Nakamura (1994) Mol. Gen. Genet. 244:563-571); the ankyrin-repeat protein family (Zhang et al. (1992) Plant Cell 4:1575-1588); the miscellaneous protein (MISC) family (Kim et al. (1997) Plant J. 11:1237-1251); the zinc finger protein (Z) family (Klug and Schwabe (1995) FASEB J. 9: 597-604); the homeobox (HB) protein family (Duboule (1994) Guidebook to the Homeobox Genes, Oxford University Press); the CAAT-element binding proteins (Forsburg and Guarente (1989) Genes Dev. 3:1166-1178); the squamosa promoter binding proteins (SPB) (Klein et al. (1996) Mol. Gen. Genet. 1996 250:7-16); the NAM protein family; the IAA/AUX proteins (Rouse et al. (1998) Science 279:1371-1373); the HLH/MYC protein family (Littlewood et al. (1994) Prot. Profile 1:639-709); the DNA-binding protein (DBP) family (Tucker et al. (1994) EMBO J. 13:2994-3002); the bZIP family of transcription factors (Foster et al. (1994) FASEB J. 8:192-200); the BPF-1 protein (Box P-binding factor) family (da Costa e Silva et al. (1993) Plant J. 4:125-135); and the golden protein (GLD) family (Hall et al. (1998) Plant Cell 10:925-936).

In addition to methods for modifying a plant phenotype by employing one or more polynucleotides and polypeptides of the invention described herein, the polynucleotides and polypeptides of the invention have a variety of additional uses. These uses include their use in the recombinant production (i.e., expression) of proteins; as regulators of plant gene expression, as diagnostic probes for the presence of complementary or partially complementary nucleic acids (including for detection of natural coding nucleic acids); as substrates for further reactions, e.g., mutation reactions, PCR reactions, or the like, of as substrates for cloning e.g., including digestion or ligation reactions, and for identifying exogenous or endogenous modulators of the transcription factors.

DEFINITIONS

A "polynucleotide" is a nucleic acid sequence comprising a plurality of polymerized nucleotide residues, e.g., at least about 15 consecutive polymerized nucleotide residues, optionally at least about 30 consecutive nucleotides, at least about 50 consecutive nucleotides. In many instances, a polynucleotide comprises a nucleotide sequence encoding a polypeptide (or protein) or a domain or fragment thereof. Additionally, the polynucleotide may comprise a promoter, an intron, an enhancer region, a polyadenylation site, a translation initiation site, 5' or 3' untranslated regions, a reporter gene, a selectable marker, or the like. The

polynucleotide can be single stranded or double stranded DNA or RNA. The polynucleotide optionally comprises modified bases or a modified backbone. The polynucleotide can be, e.g., genomic DNA or RNA, a transcript (such as an mRNA), a cDNA, a PCR product, a cloned DNA, a synthetic DNA or RNA, or the like. The polynucleotide can comprise a sequence in either
5 sense or antisense orientations.

A "recombinant polynucleotide" is a polynucleotide that is not in its native state, e.g., the polynucleotide comprises a nucleotide sequence not found in nature, or the polynucleotide is in a context other than that in which it is naturally found, e.g., separated from nucleotide sequences with which it typically is in proximity in nature, or adjacent (or contiguous
10 with) nucleotide sequences with which it typically is not in proximity. For example, the sequence at issue can be cloned into a vector, or otherwise recombined with one or more additional nucleic acid.

An "isolated polynucleotide" is a polynucleotide whether naturally occurring or recombinant, that is present outside the cell in which it is typically found in nature, whether
15 purified or not. Optionally, an isolated polynucleotide is subject to one or more enrichment or purification procedures, e.g., cell lysis, extraction, centrifugation, precipitation, or the like.

A "recombinant polypeptide" is a polypeptide produced by translation of a recombinant polynucleotide. An "isolated polypeptide," whether a naturally occurring or a recombinant polypeptide, is more enriched in (or out of) a cell than the polypeptide in its natural
20 state in a wild type cell, e.g., more than about 5% enriched, more than about 10% enriched, or more than about 20%, or more than about 50%, or more, enriched, i.e., alternatively denoted: 105%, 110%, 120%, 150% or more, enriched relative to wild type standardized at 100%. Such an enrichment is not the result of a natural response of a wild type plant. Alternatively, or additionally, the isolated polypeptide is separated from other cellular components with which it is
25 typically associated, e.g., by any of the various protein purification methods herein.

The term "transgenic plant" refers to a plant that contains genetic material, not found in a wild type plant of the same species, variety or cultivar. The genetic material may include a transgene, an insertional mutagenesis event (such as by transposon or T-DNA insertional mutagenesis), an activation tagging sequence, a mutated sequence, a homologous
30 recombination event or a sequence modified by chimeraplasty. Typically, the foreign genetic material has been introduced into the plant by human manipulation.

A transgenic plant may contain an expression vector or cassette. The expression cassette typically comprises a polypeptide-encoding sequence operably linked (i.e., under regulatory control of) to appropriate inducible or constitutive regulatory sequences that allow for

the expression of polypeptide. The expression cassette can be introduced into a plant by transformation or by breeding after transformation of a parent plant. A plant refers to a whole plant as well as to a plant part, such as seed, fruit, leaf, or root, plant tissue, plant cells or any other plant material, e.g., a plant explant, as well as to progeny thereof, and to *in vitro* systems that mimic biochemical or cellular components or processes in a cell.

The phrase "ectopically expression or altered expression" in reference to a polynucleotide indicates that the pattern of expression in, e.g., a transgenic plant or plant tissue, is different from the expression pattern in a wild type plant or a reference plant of the same species. For example, the polynucleotide or polypeptide is expressed in a cell or tissue type other than a cell or tissue type in which the sequence is expressed in the wild type plant, or by expression at a time other than at the time the sequence is expressed in the wild type plant, or by a response to different inducible agents, such as hormones or environmental signals, or at different expression levels (either higher or lower) compared with those found in a wild type plant. The term also refers to altered expression patterns that are produced by lowering the levels of expression to below the detection level or completely abolishing expression. The resulting expression pattern can be transient or stable, constitutive or inducible. In reference to a polypeptide, the term "ectopic expression or altered expression" further may relate to altered activity levels resulting from the interactions of the polypeptides with exogenous or endogenous modulators or from interactions with factors or as a result of the chemical modification of the polypeptides.

The term "fragment" or "domain," with respect to a polypeptide, refers to a subsequence of the polypeptide. In some cases, the fragment or domain, is a subsequence of the polypeptide which performs at least one biological function of the intact polypeptide in substantially the same manner, or to a similar extent, as does the intact polypeptide. For example, a polypeptide fragment can comprise a recognizable structural motif or functional domain such as a DNA binding domain that binds to a DNA promoter region, an activation domain or a domain for protein-protein interactions. Fragments can vary in size from as few as 6 amino acids to the full length of the intact polypeptide, but are preferably at least about 30 amino acids in length and more preferably at least about 60 amino acids in length. In reference to a nucleotide sequence, "a fragment" refers to any subsequence of a polynucleotide, typically, of at least consecutive about 15 nucleotides, preferably at least about 30 nucleotides, more preferably at least about 50, of any of the sequences provided herein.

The term "trait" refers to a physiological, morphological, biochemical or physical characteristic of a plant or particular plant material or cell. In some instances, this characteristic is visible to the human eye, such as seed or plant size, or can be measured by available

biochemical techniques, such as the protein, starch or oil content of seed or leaves or by the observation of the expression level of genes, e.g., by employing Northern analysis, RT-PCR, microarray gene expression assays or reporter gene expression systems, or by agricultural observations such as stress tolerance, yield or pathogen tolerance.

5 “Trait modification” refers to a detectable difference in a characteristic in a plant ectopically expressing a polynucleotide or polypeptide of the present invention relative to a plant not doing so, such as a wild type plant. In some cases, the trait modification can be evaluated quantitatively. For example, the trait modification can entail at least about a 2% increase or decrease in an observed trait (difference), at least a 5% difference, at least about a 10%
10 difference, at least about a 20% difference, at least about a 30%, at least about a 50%, at least about a 70%, or at least about a 100%, or an even greater difference. It is known that there can be a natural variation in the modified trait. Therefore, the trait modification observed entails a change of the normal distribution of the trait in the plants compared with the distribution observed in wild type plant.

15 Trait modifications of particular interest include those to seed (such as embryo or endosperm), fruit, root, flower, leaf, stem, shoot, seedling or the like, including: enhanced tolerance to environmental conditions including freezing, chilling, heat, drought, water saturation, radiation and ozone; improved tolerance to microbial, fungal or viral diseases; improved tolerance to pest infestations, including nematodes, mollicutes, parasitic higher plants or the like;
20 decreased herbicide sensitivity; improved tolerance of heavy metals or enhanced ability to take up heavy metals; improved growth under poor photoconditions (e.g., low light and/or short day length), or changes in expression levels of genes of interest. Other phenotype that can be modified relate to the production of plant metabolites, such as variations in the production of taxol, tocopherol, tocotrienol, sterols, phytosterols, vitamins, wax monomers, anti-oxidants,
25 amino acids, lignins, cellulose, tannins, prenyl lipids (such as chlorophylls and carotenoids), glucosinolates, and terpenoids, enhanced or compositionally altered protein or oil production (especially in seeds), or modified sugar (insoluble or soluble) and/or starch composition.

Physical plant characteristics that can be modified include cell development (such as the number of trichomes), fruit and seed size and number, yields of plant parts such as stems, leaves and
30 roots, the stability of the seeds during storage, characteristics of the seed pod (e.g., susceptibility to shattering), root hair length and quantity, internode distances, or the quality of seed coat. Plant growth characteristics that can be modified include growth rate, germination rate of seeds, vigor of plants and seedlings, leaf and flower senescence, male sterility, apomixis, flowering time, flower abscission, rate of nitrogen uptake, biomass or transpiration characteristics, as well as

plant architecture characteristics such as apical dominance, branching patterns, number of organs, organ identity, organ shape or size.

POLYPEPTIDES AND POLYNUCLEOTIDES OF THE INVENTION

5 The present invention provides, among other things, transcription factors (TFs), and transcription factor homologue polypeptides, and isolated or recombinant polynucleotides encoding the polypeptides. These polypeptides and polynucleotides may be employed to modify a plant's structure and development characteristics.

10 Exemplary polynucleotides encoding the polypeptides of the invention were identified in the *Arabidopsis thaliana* GenBank database using publicly available sequence analysis programs and parameters. Sequences initially identified were then further characterized to identify sequences comprising specified sequence strings corresponding to sequence motifs present in families of known transcription factors. Polynucleotide sequences meeting such criteria were confirmed as transcription factors.

15 Additional polynucleotides of the invention were identified by screening *Arabidopsis thaliana* and/or other plant cDNA libraries with probes corresponding to known transcription factors under low stringency hybridization conditions. Additional sequences, including full length coding sequences were subsequently recovered by the rapid amplification of cDNA ends (RACE) procedure, using a commercially available kit according to the manufacturer's instructions. Where necessary, multiple rounds of RACE are performed to isolate 20 5' and 3' ends. The full length cDNA was then recovered by a routine end-to-end polymerase chain reaction (PCR) using primers specific to the isolated 5' and 3' ends. Exemplary sequences are provided in the Sequence Listing.

The polynucleotides of the invention were ectopically expressed in overexpressor or knockout plants and changes in the structure and development characteristics of the plants 25 were observed. Therefore, the polynucleotides and polypeptides can be employed to improve the structure and development characteristics of plants.

Making polynucleotides

30 The polynucleotides of the invention include sequences that encode transcription factors and transcription factor homologue polypeptides and sequences complementary thereto, as well as unique fragments of coding sequence, or sequence complementary thereto. Such polynucleotides can be, e.g., DNA or RNA, e.g., mRNA, cRNA, synthetic RNA, genomic DNA, cDNA synthetic DNA, oligonucleotides, etc. The polynucleotides are either double-stranded or single-stranded, and include either, or both sense (i.e., coding) sequences and antisense (i.e., non-

coding, complementary) sequences. The polynucleotides include the coding sequence of a transcription factor, or transcription factor homologue polypeptide, in isolation, in combination with additional coding sequences (e.g., a purification tag, a localization signal, as a fusion-protein, as a pre-protein, or the like), in combination with non-coding sequences (e.g., introns or
5 inteins, regulatory elements such as promoters, enhancers, terminators, and the like), and/or in a vector or host environment in which the polynucleotide encoding a transcription factor or transcription factor homologue polypeptide is an endogenous or exogenous gene.

A variety of methods exist for producing the polynucleotides of the invention. Procedures for identifying and isolating DNA clones are well known to those of skill in the art, and are described in, e.g., Berger and Kimmel, Guide to Molecular Cloning Techniques, Methods
10 in Enzymology volume 152 Academic Press, Inc., San Diego, CA ("Berger"); Sambrook et al., Molecular Cloning - A Laboratory Manual (2nd Ed.), Vol. 1-3, Cold Spring Harbor Laboratory, Cold Spring Harbor, New York, 1989 ("Sambrook") and Current Protocols in Molecular Biology, F.M. Ausubel et al., eds., Current Protocols, a joint venture between Greene Publishing
15 Associates, Inc. and John Wiley & Sons, Inc., (supplemented through 2000) ("Ausubel").

Alternatively, polynucleotides of the invention, can be produced by a variety of in vitro amplification methods adapted to the present invention by appropriate selection of specific or degenerate primers. Examples of protocols sufficient to direct persons of skill through in vitro amplification methods, including the polymerase chain reaction (PCR) the ligase chain
20 reaction (LCR), Qbeta-replicase amplification and other RNA polymerase mediated techniques (e.g., NASBA), e.g., for the production of the homologous nucleic acids of the invention are found in Berger, Sambrook, and Ausubel, as well as Mullis et al., (1987) PCR Protocols A Guide to Methods and Applications (Innis et al. eds) Academic Press Inc. San Diego, CA (1990) (Innis). Improved methods for cloning in vitro amplified nucleic acids are described in Wallace et al.,
25 U.S. Pat. No. 5,426,039. Improved methods for amplifying large nucleic acids by PCR are summarized in Cheng et al. (1994) Nature 369: 684-685 and the references cited therein, in which PCR amplicons of up to 40kb are generated. One of skill will appreciate that essentially any RNA can be converted into a double stranded DNA suitable for restriction digestion, PCR expansion and sequencing using reverse transcriptase and a polymerase. See, e.g., Ausubel,
30 Sambrook and Berger, *all supra*.

Alternatively, polynucleotides and oligonucleotides of the invention can be assembled from fragments produced by solid-phase synthesis methods. Typically, fragments of up to approximately 100 bases are individually synthesized and then enzymatically or chemically ligated to produce a desired sequence, e.g., a polynucleotide encoding all or part of a

transcription factor. For example, chemical synthesis using the phosphoramidite method is described, e.g., by Beaucage et al. (1981) Tetrahedron Letters 22:1859-69; and Matthes et al. (1984) EMBO J. 3:801-5. According to such methods, oligonucleotides are synthesized, purified, annealed to their complementary strand, ligated and then optionally cloned into suitable vectors.

- 5 And if so desired, the polynucleotides and polypeptides of the invention can be custom ordered from any of a number of commercial suppliers.

HOMOLOGOUS SEQUENCES

- Sequences homologous, i.e., that share significant sequence identity or similarity, to those provided in the Sequence Listing, derived from *Arabidopsis thaliana* or from other plants of choice are also an aspect of the invention. Homologous sequences can be derived from any plant including monocots and dicots and in particular agriculturally important plant species, including but not limited to, crops such as soybean, wheat, corn, potato, cotton, rice, oilseed rape (including canola), sunflower, alfalfa, sugarcane and turf; or fruits and vegetables, such as banana, blackberry, blueberry, strawberry, and raspberry, cantaloupe, carrot, cauliflower, coffee, cucumber, eggplant, grapes, honeydew, lettuce, mango, melon, onion, papaya, peas, peppers, pineapple, spinach, squash, sweet corn, tobacco, tomato, watermelon, rosaceous fruits (such as apple, peach, pear, cherry and plum) and vegetable brassicas (such as broccoli, cabbage, cauliflower, brussel sprouts and kohlrabi). Other crops, fruits and vegetables whose phenotype can be changed include barley, rye, millet, sorghum, currant, avocado, citrus fruits such as oranges, lemons, grapefruit and tangerines, artichoke, cherries, nuts such as the walnut and peanut, endive, leek, roots, such as arrowroot, beet, cassava, turnip, radish, yam, and sweet potato, and beans. The homologous sequences may also be derived from woody species, such as pine, poplar and eucalyptus.

- Transcription factors that are homologous to the listed sequences will typically share at least about 30% amino acid sequence identity. More closely related transcription factors can share at least about 50%, about 60%, about 65%, about 70%, about 75% or about 80% or about 90% or about 95% or about 98% or more sequence identity with the listed sequences. Factors that are most closely related to the listed sequences share, e.g., at least about 85%, about 90% or about 95% or more % sequence identity to the listed sequences. At the nucleotide level, the sequences will typically share at least about 40% nucleotide sequence identity, preferably at least about 50%, about 60%, about 70% or about 80% sequence identity, and more preferably about 85%, about 90%, about 95% or about 97% or more sequence identity to one or more of the listed sequences. The degeneracy of the genetic code enables major variations in the nucleotide

sequence of a polynucleotide while maintaining the amino acid sequence of the encoded protein. Conserved domains within a transcription factor family may exhibit a higher degree of sequence homology, such as at least 65% sequence identity including conservative substitutions, and preferably at least 80% sequence identity.

5 Identifying Nucleic Acids by Hybridization

Polynucleotides homologous to the sequences illustrated in the Sequence Listing can be identified, e.g., by hybridization to each other under stringent or under highly stringent conditions. Single stranded polynucleotides hybridize when they associate based on a variety of well characterized physico-chemical forces, such as hydrogen bonding, solvent exclusion, base
10 stacking and the like. The stringency of a hybridization reflects the degree of sequence identity of the nucleic acids involved, such that the higher the stringency, the more similar are the two polynucleotide strands. Stringency is influenced by a variety of factors, including temperature, salt concentration and composition, organic and non-organic additives, solvents, etc. present in both the hybridization and wash solutions and incubations (and number), as described in more
15 detail in the references cited above.

An example of stringent hybridization conditions for hybridization of complementary nucleic acids which have more than 100 complementary residues on a filter in a Southern or northern blot is about 5°C to 20°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength and pH. The T_m is the temperature (under defined
20 ionic strength and pH) at which 50% of the target sequence hybridizes to a perfectly matched probe. Nucleic acid molecules that hybridize under stringent conditions will typically hybridize to a probe based on either the entire cDNA or selected portions, e.g., to a unique subsequence, of the cDNA under wash conditions of 0.2x SSC to 2.0 x SSC, 0.1% SDS at 50-65° C, for example 0.2 x SSC, 0.1% SDS at 65° C. For identification of less closely related homologues washes can
25 be performed at a lower temperature, e.g., 50° C. In general, stringency is increased by raising the wash temperature and/or decreasing the concentration of SSC.

As another example, stringent conditions can be selected such that an oligonucleotide that is perfectly complementary to the coding oligonucleotide hybridizes to the coding oligonucleotide with at least about a 5-10x higher signal to noise ratio than the ratio for
30 hybridization of the perfectly complementary oligonucleotide to a nucleic acid encoding a transcription factor known as of the filing date of the application. Conditions can be selected such that a higher signal to noise ratio is observed in the particular assay which is used, e.g., about 15x, 25x, 35x, 50x or more. Accordingly, the subject nucleic acid hybridizes to the unique coding oligonucleotide with at least a 2x higher signal to noise ratio as compared to hybridization

of the coding oligonucleotide to a nucleic acid encoding known polypeptide. Again, higher signal to noise ratios can be selected, e.g., about 5x, 10x, 25x, 35x, 50x or more. The particular signal will depend on the label used in the relevant assay, e.g., a fluorescent label, a colorimetric label, a radio active label, or the like.

5 Alternatively, transcription factor homologue polypeptides can be obtained by screening an expression library using antibodies specific for one or more transcription factors. With the provision herein of the disclosed transcription factor, and transcription factor homologue nucleic acid sequences, the encoded polypeptide(s) can be expressed and purified in a heterologous expression system (e.g., *E. coli*) and used to raise antibodies (monoclonal or
10 polyclonal) specific for the polypeptide(s) in question. Antibodies can also be raised against synthetic peptides derived from transcription factor, or transcription factor homologue, amino acid sequences. Methods of raising antibodies are well known in the art and are described in Harlow and Lane (1988) Antibodies: A Laboratory Manual, Cold Spring Harbor Laboratory, New
15 York. Such antibodies can then be used to screen an expression library produced from the plant from which it is desired to clone additional transcription factor homologues, using the methods described above. The selected cDNAs can be confirmed by sequencing and enzymatic activity.

SEQUENCE VARIATIONS

It will readily be appreciated by those of skill in the art, that any of a variety of polynucleotide sequences are capable of encoding the transcription factors and transcription
20 factor homologue polypeptides of the invention. Due to the degeneracy of the genetic code, many different polynucleotides can encode identical and/or substantially similar polypeptides in addition to those sequences illustrated in the Sequence Listing.

For example, Table 1 illustrates, e.g., that the codons AGC, AGT, TCA, TCC, TCG, and TCT all encode the same amino acid: serine. Accordingly, at each position in the
25 sequence where there is a codon encoding serine, any of the above trinucleotide sequences can be used without altering the encoded polypeptide.

Table 1

Amino acids			Codon						
Alanine	Ala	A	GCA	GCC	GCG	GCU			
Cysteine	Cys	C	TGC	TGT					
Aspartic acid	Asp	D	GAC	GAT					
Glutamic acid	Glu	E	GAA	GAG					
Phenylalanine	Phe	F	TTC	TTT					
Glycine	Gly	G	GGA	GGC	GGG	GGT			
Histidine	His	H	CAC	CAT					
Isoleucine	Ile	I	ATA	ATC	ATT				
Lysine	Lys	K	AAA	AAG					
Leucine	Leu	L	TTA	TTG	CTA	CTC	CTG	CTT	
Methionine	Met	M	ATG						
Asparagine	Asn	N	AAC	AAT					
Proline	Pro	P	CCA	CCC	CCG	CCT			
Glutamine	Gln	Q	CAA	CAG					
Arginine	Arg	R	AGA	AGG	CGA	CGC	CGG	CGT	
Serine	Ser	S	AGC	AGT	TCA	TCC	TCG	TCT	
Threonine	Thr	T	ACA	ACC	ACG	ACT			
Valine	Val	V	GTA	GTC	GTG	GTT			
Tryptophan	Trp	W	TGG						
Tyrosine	Tyr	Y	TAC	TAT					

Sequence alterations that do not change the amino acid sequence encoded by the polynucleotide are termed "silent" variations. With the exception of the codons ATG and TGG, encoding methionine and tryptophan, respectively, any of the possible codons for the same amino acid can be substituted by a variety of techniques, e.g., site-directed mutagenesis, available in the art. Accordingly, any and all such variations of a sequence selected from the above table are a feature of the invention.

In addition to silent variations, other conservative variations that alter one, or a few amino acids in the encoded polypeptide, can be made without altering the function of the polypeptide, these conservative variants are, likewise, a feature of the invention.

For example, substitutions, deletions and insertions introduced into the sequences provided in the Sequence Listing are also envisioned by the invention. Such sequence modifications can be engineered into a sequence by site-directed mutagenesis (Wu (ed.) Meth. Enzymol. (1993) vol. 217, Academic Press) or the other methods noted below. Amino acid substitutions are typically of single residues; insertions usually will be on the order of about from 1 to 10 amino acid residues; and deletions will range about from 1 to 30 residues. In preferred embodiments, deletions or insertions are made in adjacent pairs, e.g., a deletion of two residues or insertion of two residues. Substitutions, deletions, insertions or any combination thereof can be

combined to arrive at a sequence. The mutations that are made in the polynucleotide encoding the transcription factor should not place the sequence out of reading frame and should not create complementary regions that could produce secondary mRNA structure. Preferably, the polypeptide encoded by the DNA performs the desired function.

- 5 Conservative substitutions are those in which at least one residue in the amino acid sequence has been removed and a different residue inserted in its place. Such substitutions generally are made in accordance with the Table 2 when it is desired to maintain the activity of the protein. Table 2 shows amino acids which can be substituted for an amino acid in a protein and which are typically regarded as conservative substitutions.

10

Table 2

Residue	Conservative Substitutions
Ala	Ser
Arg	Lys
Asn	Gln; His
Asp	Glu
Gln	Asn
Cys	Ser
Glu	Asp
Gly	Pro
His	Asn; Gln
Ile	Leu, Val
Leu	Ile; Val
Lys	Arg; Gln
Met	Leu; Ile
Phe	Met; Leu; Tyr
Ser	Thr; Gly
Thr	Ser; Val
Trp	Tyr
Tyr	Trp; Phe
Val	Ile; Leu

Substitutions that are less conservative than those in Table 2 can be selected by picking residues that differ more significantly in their effect on maintaining (a) the structure of

the polypeptide backbone in the area of the substitution, for example, as a sheet or helical conformation, (b) the charge or hydrophobicity of the molecule at the target site, or (c) the bulk of the side chain. The substitutions which in general are expected to produce the greatest changes in protein properties will be those in which (a) a hydrophilic residue, e.g., seryl or threonyl, is substituted for (or by) a hydrophobic residue, e.g., leucyl, isoleucyl, phenylalanyl, valyl or alanyl; (b) a cysteine or proline is substituted for (or by) any other residue; (c) a residue having an electropositive side chain, e.g., lysyl, arginyl, or histidyl, is substituted for (or by) an electronegative residue, e.g., glutamyl or aspartyl; or (d) a residue having a bulky side chain, e.g., phenylalanine, is substituted for (or by) one not having a side chain, e.g., glycine.

10 FURTHER MODIFYING SEQUENCES OF THE INVENTION—MUTATION/ FORCED EVOLUTION

In addition to generating silent or conservative substitutions as noted, above, the present invention optionally includes methods of modifying the sequences of the Sequence Listing. In the methods, nucleic acid or protein modification methods are used to alter the given sequences to produce new sequences and/or to chemically or enzymatically modify given sequences to change the properties of the nucleic acids or proteins.

Thus, in one embodiment, given nucleic acid sequences are modified, e.g., according to standard mutagenesis or artificial evolution methods to produce modified sequences. For example, Ausubel, *supra*, provides additional details on mutagenesis methods. Artificial forced evolution methods are described, e.g., by Stemmer (1994) *Nature* 370:389-391, and Stemmer (1994) *Proc. Natl. Acad. Sci. USA* 91:10747-10751. Many other mutation and evolution methods are also available and expected to be within the skill of the practitioner.

Similarly, chemical or enzymatic alteration of expressed nucleic acids and polypeptides can be performed by standard methods. For example, sequence can be modified by addition of lipids, sugars, peptides, organic or inorganic compounds, by the inclusion of modified nucleotides or amino acids, or the like. For example, protein modification techniques are illustrated in Ausubel, *supra*. Further details on chemical and enzymatic modifications can be found herein. These modification methods can be used to modify any given sequence, or to modify any sequence produced by the various mutation and artificial evolution modification methods noted herein.

Accordingly, the invention provides for modification of any given nucleic acid by mutation, evolution, chemical or enzymatic modification, or other available methods, as well as for the products produced by practicing such methods, e.g., using the sequences herein as a starting substrate for the various modification approaches.

For example, optimized coding sequence containing codons preferred by a particular prokaryotic or eukaryotic host can be used e.g., to increase the rate of translation or to produce recombinant RNA transcripts having desirable properties, such as a longer half-life, as compared with transcripts produced using a non-optimized sequence. Translation stop codons can also be modified to reflect host preference. For example, preferred stop codons for *S. cerevisiae* and mammals are TAA and TGA, respectively. The preferred stop codon for monocotyledonous plants is TGA, whereas insects and *E. coli* prefer to use TAA as the stop codon.

The polynucleotide sequences of the present invention can also be engineered in order to alter a coding sequence for a variety of reasons, including but not limited to, alterations which modify the sequence to facilitate cloning, processing and/or expression of the gene product. For example, alterations are optionally introduced using techniques which are well known in the art, e.g., site-directed mutagenesis, to insert new restriction sites, to alter glycosylation patterns, to change codon preference, to introduce splice sites, etc.

Furthermore, a fragment or domain derived from any of the polypeptides of the invention can be combined with domains derived from other transcription factors or synthetic domains to modify the biological activity of a transcription factor. For instance, a DNA binding domain derived from a transcription factor of the invention can be combined with the activation domain of another transcription factor or with a synthetic activation domain. A transcription activation domain assists in initiating transcription from a DNA binding site. Examples include the transcription activation region of VP16 or GAL4 (Moore et al. (1998) Proc. Natl. Acad. Sci. USA 95: 376-381; and Aoyama et al. (1995) Plant Cell 7:1773-1785), peptides derived from bacterial sequences (Ma and Ptashne (1987) Cell 51; 113-119) and synthetic peptides (Giniger and Ptashne, (1987) Nature 330:670-672).

EXPRESSION AND MODIFICATION OF POLYPEPTIDES

Typically, polynucleotide sequences of the invention are incorporated into recombinant DNA (or RNA) molecules that direct expression of polypeptides of the invention in appropriate host cells, transgenic plants, in vitro translation systems, or the like. Due to the inherent degeneracy of the genetic code, nucleic acid sequences which encode substantially the same or a functionally equivalent amino acid sequence can be substituted for any listed sequence to provide for cloning and expressing the relevant homologue.

Vectors, Promoters and Expression Systems

The present invention includes recombinant constructs comprising one or more of the nucleic acid sequences herein. The constructs typically comprise a vector, such as a plasmid, a cosmid, a phage, a virus (e.g., a plant virus), a bacterial artificial chromosome (BAC),
5 a yeast artificial chromosome (YAC), or the like, into which a nucleic acid sequence of the invention has been inserted, in a forward or reverse orientation. In a preferred aspect of this embodiment, the construct further comprises regulatory sequences, including, for example, a promoter, operably linked to the sequence. Large numbers of suitable vectors and promoters are known to those of skill in the art, and are commercially available.

10 General texts which describe molecular biological techniques useful herein, including the use and production of vectors, promoters and many other relevant topics, include Berger, Sambrook and Ausubel, *supra*. Any of the identified sequences can be incorporated into a cassette or vector, e.g., for expression in plants. A number of expression vectors suitable for stable transformation of plant cells or for the establishment of transgenic plants have been described
15 including those described in Weissbach and Weissbach, (1989) Methods for Plant Molecular Biology, Academic Press, and Gelvin et al., (1990) Plant Molecular Biology Manual, Kluwer Academic Publishers. Specific examples include those derived from a Ti plasmid of *Agrobacterium tumefaciens*, as well as those disclosed by Herrera-Estrella et al. (1983) Nature 303: 209, Bevan (1984) Nucl Acid Res. 12: 8711-8721, Klee (1985) Bio/Technology 3: 637-642,
20 for dicotyledonous plants.

Alternatively, non-Ti vectors can be used to transfer the DNA into monocotyledonous plants and cells by using free DNA delivery techniques. Such methods can involve, for example, the use of liposomes, electroporation, microprojectile bombardment, silicon carbide whiskers, and viruses. By using these methods transgenic plants such as wheat, rice
25 (Christou (1991) Bio/Technology 9: 957-962) and corn (Gordon-Kamm (1990) Plant Cell 2: 603-618) can be produced. An immature embryo can also be a good target tissue for monocots for direct DNA delivery techniques by using the particle gun (Weeks et al. (1993) Plant Physiol 102: 1077-1084; Vasil (1993) Bio/Technology 10: 667-674; Wan and Lemeaux (1994) Plant Physiol 104: 37-48, and for *Agrobacterium*-mediated DNA transfer (Ishida et al. (1996) Nature Biotech
30 14: 745-750).

Typically, plant transformation vectors include one or more cloned plant coding sequence (genomic or cDNA) under the transcriptional control of 5' and 3' regulatory sequences and a dominant selectable marker. Such plant transformation vectors typically also contain a promoter (e.g., a regulatory region controlling inducible or constitutive, environmentally-or

developmentally-regulated, or cell- or tissue-specific expression), a transcription initiation start site, an RNA processing signal (such as intron splice sites), a transcription termination site, and/or a polyadenylation signal.

- Examples of constitutive plant promoters which can be useful for expressing the
- 5 TF sequence include: the cauliflower mosaic virus (CaMV) 35S promoter, which confers constitutive, high-level expression in most plant tissues (*see, e.g.,* Odel et al. (1985) Nature 313:810); the nopaline synthase promoter (An et al. (1988) Plant Physiol 88:547); and the octopine synthase promoter (Fromm et al. (1989) Plant Cell 1: 977).

- A variety of plant gene promoters that regulate gene expression in response to
- 10 environmental, hormonal, chemical, developmental signals, and in a tissue-active manner can be used for expression of a TF sequence in plants. Choice of a promoter is based largely on the phenotype of interest and is determined by such factors as tissue (e.g., seed, fruit, root, pollen, vascular tissue, flower, carpel, etc.), inducibility (e.g., in response to wounding, heat, cold, drought, light, pathogens, etc.), timing, developmental stage, and the like. Numerous known
- 15 promoters have been characterized and can favorably be employed to promote expression of a polynucleotide of the invention in a transgenic plant or cell of interest. For example, tissue specific promoters include: seed-specific promoters (such as the napin, phaseolin or DC3 promoter described in US Pat. No. 5,773,697), fruit-specific promoters that are active during fruit ripening (such as the dru 1 promoter (US Pat. No. 5,783,393), or the 2A11 promoter (US Pat. No.
- 20 4,943,674) and the tomato polygalacturonase promoter (Bird et al. (1988) Plant Mol Biol 11:651), root-specific promoters, such as those disclosed in US Patent Nos. 5,618,988, 5,837,848 and 5,905,186, pollen-active promoters such as PTA29, PTA26 and PTA13 (US Pat. No. 5,792,929), promoters active in vascular tissue (Ringli and Keller (1998) Plant Mol Biol 37:977-988), flower-specific (Kaiser et al. (1995) Plant Mol Biol 28:231-243), pollen (Baerson et al. (1994) Plant Mol
- 25 Biol 26:1947-1959), carpels (Ohl et al. (1990) Plant Cell 2:837-848), pollen and ovules (Baerson et al. (1993) Plant Mol Biol 22:255-267), auxin-inducible promoters (such as that described in van der Kop et al. (1999) Plant Mol Biol 39:979-990 or Baumann et al. (1999) Plant Cell 11:323-334), cytokinin-inducible promoter (Guevara-Garcia (1998) Plant Mol Biol 38:743-753), promoters responsive to gibberellin (Shi et al. (1998) Plant Mol Biol 38:1053-1060, Willmott et
- 30 al. (1998) 38:817-825) and the like. Additional promoters are those that elicit expression in response to heat (Ainley et al. (1993) Plant Mol Biol 22: 13-23), light (e.g., the pea rbcS-3A promoter, Kuhlemeier et al. (1989) Plant Cell 1:471, and the maize rbcS promoter, Schaffner and Sheen (1991) Plant Cell 3: 997); wounding (e.g., *wun1*, Siebertz et al. (1989) Plant Cell 1: 961); pathogens (such as the PR-1 promoter described in Buchel et al. (1999) Plant Mol. Biol. 40:387-

396, and the PDF1.2 promoter described in Manners et al. (1998) Plant Mol. Biol. 38:1071-80), and chemicals such as methyl jasmonate or salicylic acid (Gatz et al. (1997) Plant Mol Biol 48: 89-108). In addition, the timing of the expression can be controlled by using promoters such as those acting at senescence (An and Amazon (1995) Science 270: 1986-1988); or late seed development (Odell et al. (1994) Plant Physiol 106:447-458).

Plant expression vectors can also include RNA processing signals that can be positioned within, upstream or downstream of the coding sequence. In addition, the expression vectors can include additional regulatory sequences from the 3'-untranslated region of plant genes, e.g., a 3' terminator region to increase mRNA stability of the mRNA, such as the PI-II terminator region of potato or the octopine or nopaline synthase 3' terminator regions.

Additional Expression Elements

Specific initiation signals can aid in efficient translation of coding sequences.

These signals can include, e.g., the ATG initiation codon and adjacent sequences. In cases where a coding sequence, its initiation codon and upstream sequences are inserted into the appropriate expression vector, no additional translational control signals may be needed. However, in cases where only coding sequence (e.g., a mature protein coding sequence), or a portion thereof, is inserted, exogenous transcriptional control signals including the ATG initiation codon can be separately provided. The initiation codon is provided in the correct reading frame to facilitate transcription. Exogenous transcriptional elements and initiation codons can be of various origins, both natural and synthetic. The efficiency of expression can be enhanced by the inclusion of enhancers appropriate to the cell system in use.

Expression Hosts

The present invention also relates to host cells which are transduced with vectors of the invention, and the production of polypeptides of the invention (including fragments thereof) by recombinant techniques. Host cells are genetically engineered (i.e, nucleic acids are introduced, e.g., transduced, transformed or transfected) with the vectors of this invention, which may be, for example, a cloning vector or an expression vector comprising the relevant nucleic acids herein. The vector is optionally a plasmid, a viral particle, a phage, a naked nucleic acids, etc. The engineered host cells can be cultured in conventional nutrient media modified as appropriate for activating promoters, selecting transformants, or amplifying the relevant gene. The culture conditions, such as temperature, pH and the like, are those previously used with the host cell selected for expression, and will be apparent to those skilled in the art and in the references cited herein, including, Sambrook and Ausubel.

The host cell can be a eukaryotic cell, such as a yeast cell, or a plant cell, or the host cell can be a prokaryotic cell, such as a bacterial cell. Plant protoplasts are also suitable for some applications. For example, the DNA fragments are introduced into plant tissues, cultured plant cells or plant protoplasts by standard methods including electroporation (Fromm et al., (1985) Proc. Natl. Acad. Sci. USA 82, 5824, infection by viral vectors such as cauliflower mosaic virus (CaMV) (Hohn et al., (1982) Molecular Biology of Plant Tumors, (Academic Press, New York) pp. 549-560; US 4,407,956), high velocity ballistic penetration by small particles with the nucleic acid either within the matrix of small beads or particles, or on the surface (Klein et al., (1987) Nature 327, 70-73), use of pollen as vector (WO 85/01856), or use of *Agrobacterium tumefaciens* or *A. rhizogenes* carrying a T-DNA plasmid in which DNA fragments are cloned. The T-DNA plasmid is transmitted to plant cells upon infection by *Agrobacterium tumefaciens*, and a portion is stably integrated into the plant genome (Horsch et al. (1984) Science 233:496-498; Fraley et al. (1983) Proc. Natl. Acad. Sci. USA 80, 4803).

The cell can include a nucleic acid of the invention which encodes a polypeptide, wherein the cells expresses a polypeptide of the invention. The cell can also include vector sequences, or the like. Furthermore, cells and transgenic plants which include any polypeptide or nucleic acid above or throughout this specification, e.g., produced by transduction of a vector of the invention, are an additional feature of the invention.

For long-term, high-yield production of recombinant proteins, stable expression can be used. Host cells transformed with a nucleotide sequence encoding a polypeptide of the invention are optionally cultured under conditions suitable for the expression and recovery of the encoded protein from cell culture. The protein or fragment thereof produced by a recombinant cell may be secreted, membrane-bound, or contained intracellularly, depending on the sequence and/or the vector used. As will be understood by those of skill in the art, expression vectors containing polynucleotides encoding mature proteins of the invention can be designed with signal sequences which direct secretion of the mature polypeptides through a prokaryotic or eukaryotic cell membrane.

Modified Amino Acids

Polypeptides of the invention may contain one or more modified amino acids.

The presence of modified amino acids may be advantageous in, for example, increasing polypeptide half-life, reducing polypeptide antigenicity or toxicity, increasing polypeptide storage stability, or the like. Amino acid(s) are modified, for example, co-translationally or post-translationally during recombinant production or modified by synthetic or chemical means.

Non-limiting examples of a modified amino acid include incorporation or other use of acetylated amino acids, glycosylated amino acids, sulfated amino acids, prenylated (e.g., farnesylated, geranylgeranylated) amino acids, PEG modified (e.g., "PEGylated") amino acids, biotinylated amino acids, carboxylated amino acids, phosphorylated amino acids, etc. References
5 adequate to guide one of skill in the modification of amino acids are replete throughout the literature.

IDENTIFICATION OF ADDITIONAL FACTORS

A transcription factor provided by the present invention can also be used to identify additional endogenous or exogenous molecules that can affect a phenotype or trait of
10 interest. On the one hand, such molecules include organic (small or large molecules) and/or inorganic compounds that affect expression of (i.e., regulate) a particular transcription factor. Alternatively, such molecules include endogenous molecules that are acted upon either at a transcriptional level by a transcription factor of the invention to modify a phenotype as desired. For example, the transcription factors can be employed to identify one or more downstream gene
15 with which is subject to a regulatory effect of the transcription factor. In one approach, a transcription factor or transcription factor homologue of the invention is expressed in a host cell, e.g., a transgenic plant cell, tissue or explant, and expression products, either RNA or protein, of likely or random targets are monitored, e.g., by hybridization to a microarray of nucleic acid probes corresponding to genes expressed in a tissue or cell type of interest, by two-dimensional
20 gel electrophoresis of protein products, or by any other method known in the art for assessing expression of gene products at the level of RNA or protein. Alternatively, a transcription factor of the invention can be used to identify promoter sequences (i.e., binding sites) involved in the regulation of a downstream target. After identifying a promoter sequence, interactions between the transcription factor and the promoter sequence can be modified by changing specific
25 nucleotides in the promoter sequence or specific amino acids in the transcription factor that interact with the promoter sequence to alter a plant trait. Typically, transcription factor DNA binding sites are identified by gel shift assays. After identifying the promoter regions, the promoter region sequences can be employed in double-stranded DNA arrays to identify molecules that affect the interactions of the transcription factors with their promoters (Bulyk et al.
30 (1999) Nature Biotechnology 17:573-577).

The identified transcription factors are also useful to identify proteins that modify the activity of the transcription factor. Such modification can occur by covalent modification, such as by phosphorylation, or by protein-protein (homo or-heteropolymer) interactions. Any

method suitable for detecting protein-protein interactions can be employed. Among the methods that can be employed are co-immunoprecipitation, cross-linking and co-purification through gradients or chromatographic columns, and the two-hybrid yeast system.

The two-hybrid system detects protein interactions in vivo and is described in Chien, et al., (1991), Proc. Natl. Acad. Sci. USA 88, 9578-9582 and is commercially available from Clontech (Palo Alto, Calif.). In such a system, plasmids are constructed that encode two hybrid proteins: one consists of the DNA-binding domain of a transcription activator protein fused to the TF polypeptide and the other consists of the transcription activator protein's activation domain fused to an unknown protein that is encoded by a cDNA that has been recombined into the plasmid as part of a cDNA library. The DNA-binding domain fusion plasmid and the cDNA library are transformed into a strain of the yeast *Saccharomyces cerevisiae* that contains a reporter gene (e.g., lacZ) whose regulatory region contains the transcription activator's binding site. Either hybrid protein alone cannot activate transcription of the reporter gene. Interaction of the two hybrid proteins reconstitutes the functional activator protein and results in expression of the reporter gene, which is detected by an assay for the reporter gene product. Then, the library plasmids responsible for reporter gene expression are isolated and sequenced to identify the proteins encoded by the library plasmids. After identifying proteins that interact with the transcription factors, assays for compounds that interfere with the TF protein-protein interactions can be preformed.

20 IDENTIFICATION OF MODULATORS

In addition to the intracellular molecules described above, extracellular molecules that alter activity or expression of a transcription factor, either directly or indirectly, can be identified. For example, the methods can entail first placing a candidate molecule in contact with a plant or plant cell. The molecule can be introduced by topical administration, such as spraying or soaking of a plant, and then the molecule's effect on the expression or activity of the TF polypeptide or the expression of the polynucleotide monitored. Changes in the expression of the TF polypeptide can be monitored by use of polyclonal or monoclonal antibodies, gel electrophoresis or the like. Changes in the expression of the corresponding polynucleotide sequence can be detected by use of microarrays, Northern, quantitative PCR, or any other technique for monitoring changes in mRNA expression. These techniques are exemplified in Ausubel et al. (eds) Current Protocols in Molecular Biology, John Wiley & Sons (1998). Such changes in the expression levels can be correlated with modified plant traits and thus identified

molecules can be useful for soaking or spraying on fruit, vegetable and grain crops to modify traits in plants.

Essentially any available composition can be tested for modulatory activity of expression or activity of any nucleic acid or polypeptide herein. Thus, available libraries of
5 compounds such as chemicals, polypeptides, nucleic acids and the like can be tested for modulatory activity. Often, potential modulator compounds can be dissolved in aqueous or organic (e.g., DMSO-based) solutions for easy delivery to the cell or plant of interest in which the activity of the modulator is to be tested. Optionally, the assays are designed to screen large modulator composition libraries by automating the assay steps and providing compounds from
10 any convenient source to assays, which are typically run in parallel (e.g., in microtiter formats on microtiter plates in robotic assays).

In one embodiment, high throughput screening methods involve providing a combinatorial library containing a large number of potential compounds (potential modulator compounds). Such "combinatorial chemical libraries" are then screened in one or more assays, as
15 described herein, to identify those library members (particular chemical species or subclasses) that display a desired characteristic activity. The compounds thus identified can serve as target compounds.

A combinatorial chemical library can be, e.g., a collection of diverse chemical compounds generated by chemical synthesis or biological synthesis. For example, a
20 combinatorial chemical library such as a polypeptide library is formed by combining a set of chemical building blocks (e.g., in one example, amino acids) in every possible way for a given compound length (i.e., the number of amino acids in a polypeptide compound of a set length). Exemplary libraries include peptide libraries, nucleic acid libraries, antibody libraries (see, e.g., Vaughn et al. (1996) Nature Biotechnology, 14(3):309-314 and PCT/US96/10287), carbohydrate
25 libraries (see, e.g., Liang et al. Science (1996) 274:1520-1522 and U.S. Patent 5,593,853), peptide nucleic acid libraries (see, e.g., U.S. Patent 5,539,083), and small organic molecule libraries (see, e.g., benzodiazepines, Baum C&EN Jan 18, page 33 (1993); isoprenoids, U.S. Patent 5,569,588; thiazolidinones and metathiazanones, U.S. Patent 5,549,974; pyrrolidines, U.S. Patents 5,525,735 and 5,519,134; morpholino compounds, U.S. Patent 5,506,337) and the like.

30 Preparation and screening of combinatorial or other libraries is well known to those of skill in the art. Such combinatorial chemical libraries include, but are not limited to, peptide libraries (see, e.g., U.S. Patent 5,010,175, Furka, Int. J. Pept. Prot. Res. 37:487-493 (1991) and Houghton et al. Nature 354:84-88 (1991)). Other chemistries for generating chemical diversity libraries can also be used.

In addition, as noted, compound screening equipment for high-throughput screening is generally available, e.g., using any of a number of well known robotic systems that have also been developed for solution phase chemistries useful in assay systems. These systems include automated workstations including an automated synthesis apparatus and robotic systems
5 utilizing robotic arms. Any of the above devices are suitable for use with the present invention, e.g., for high-throughput screening of potential modulators. The nature and implementation of modifications to these devices (if any) so that they can operate as discussed herein will be apparent to persons skilled in the relevant art.

Indeed, entire high throughput screening systems are commercially available.
10 These systems typically automate entire procedures including all sample and reagent pipetting, liquid dispensing, timed incubations, and final readings of the microplate in detector(s) appropriate for the assay. These configurable systems provide high throughput and rapid start up as well as a high degree of flexibility and customization. Similarly, microfluidic implementations of screening are also commercially available.

15 The manufacturers of such systems provide detailed protocols the various high throughput. Thus, for example, Zymark Corp. provides technical bulletins describing screening systems for detecting the modulation of gene transcription, ligand binding, and the like. The integrated systems herein, in addition to providing for sequence alignment and, optionally, synthesis of relevant nucleic acids, can include such screening apparatus to identify modulators
20 that have an effect on one or more polynucleotides or polypeptides according to the present invention.

In some assays it is desirable to have positive controls to ensure that the components of the assays are working properly. At least two types of positive controls are appropriate. That is, known transcriptional activators or inhibitors can be incubated with
25 cells/plants/ etc. in one sample of the assay, and the resulting increase/decrease in transcription can be detected by measuring the resulting increase in RNA/ protein expression, etc., according to the methods herein. It will be appreciated that modulators can also be combined with transcriptional activators or inhibitors to find modulators which inhibit transcriptional activation or transcriptional repression. Either expression of the nucleic acids and proteins herein or any
30 additional nucleic acids or proteins activated by the nucleic acids or proteins herein, or both, can be monitored.

In an embodiment, the invention provides a method for identifying compositions that modulate the activity or expression of a polynucleotide or polypeptide of the invention. For example, a test compound, whether a small or large molecule, is placed in contact with a cell,

plant (or plant tissue or explant), or composition comprising the polynucleotide or polypeptide of interest and a resulting effect on the cell, plant, (or tissue or explant) or composition is evaluated by monitoring, either directly or indirectly, one or more of: expression level of the polynucleotide or polypeptide, activity (or modulation of the activity) of the polynucleotide or polypeptide. In some cases, an alteration in a plant phenotype can be detected following contact of a plant (or plant cell, or tissue or explant) with the putative modulator, e.g., by modulation of expression or activity of a polynucleotide or polypeptide of the invention.

SUBSEQUENCES

Also contemplated are uses of polynucleotides, also referred to herein as oligonucleotides, typically having at least 12 bases, preferably at least 15, more preferably at least 20, 30, or 50 bases, which hybridize under at least highly stringent (or ultra-high stringent or ultra-ultra- high stringent conditions) conditions to a polynucleotide sequence described above. The polynucleotides may be used as probes, primers, sense and antisense agents, and the like, according to methods as noted *supra*.

Subsequences of the polynucleotides of the invention, including polynucleotide fragments and oligonucleotides are useful as nucleic acid probes and primers. An oligonucleotide suitable for use as a probe or primer is at least about 15 nucleotides in length, more often at least about 18 nucleotides, often at least about 21 nucleotides, frequently at least about 30 nucleotides, or about 40 nucleotides, or more in length. A nucleic acid probe is useful in hybridization protocols, e.g., to identify additional polypeptide homologues of the invention, including protocols for microarray experiments. Primers can be annealed to a complementary target DNA strand by nucleic acid hybridization to form a hybrid between the primer and the target DNA strand, and then extended along the target DNA strand by a DNA polymerase enzyme. Primer pairs can be used for amplification of a nucleic acid sequence, e.g., by the polymerase chain reaction (PCR) or other nucleic-acid amplification methods. See Sambrook and Ausubel, *supra*.

In addition, the invention includes an isolated or recombinant polypeptide including a subsequence of at least about 15 contiguous amino acids encoded by the recombinant or isolated polynucleotides of the invention. For example, such polypeptides, or domains or fragments thereof, can be used as immunogens, e.g., to produce antibodies specific for the polypeptide sequence, or as probes for detecting a sequence of interest. A subsequence can range in size from about 15 amino acids in length up to and including the full length of the polypeptide.

PRODUCTION OF TRANSGENIC PLANTS

Modification of Traits

The polynucleotides of the invention are favorably employed to produce transgenic plants with various traits, or characteristics, that have been modified in a desirable manner, e.g., to improve the seed characteristics of a plant. For example, alteration of expression levels or patterns (e.g., spatial or temporal expression patterns) of one or more of the transcription factors (or transcription factor homologues) of the invention, as compared with the levels of the same protein found in a wild type plant, can be used to modify a plant's traits. An illustrative example of trait modification, modified structure and development characteristics, by altering expression levels of a particular transcription factor is described further in the Examples and the Sequence Listing.

Antisense and Cosuppression Approaches

In addition to expression of the nucleic acids of the invention as gene replacement or plant phenotype modification nucleic acids, the nucleic acids are also useful for sense and anti-sense suppression of expression, e.g., to down-regulate expression of a nucleic acid of the invention, e.g., as a further mechanism for modulating plant phenotype. That is, the nucleic acids of the invention, or subsequences or anti-sense sequences thereof, can be used to block expression of naturally occurring homologous nucleic acids. A variety of sense and anti-sense technologies are known in the art, e.g., as set forth in Lichtenstein and Nellen (1997) Antisense Technology: A Practical Approach IRL Press at Oxford University, Oxford, England. In general, sense or anti-sense sequences are introduced into a cell, where they are optionally amplified, e.g., by transcription. Such sequences include both simple oligonucleotide sequences and catalytic sequences such as ribozymes.

For example, a reduction or elimination of expression (i.e., a "knock-out") of a transcription factor or transcription factor homologue polypeptide in a transgenic plant, e.g., to modify a plant trait, can be obtained by introducing an antisense construct corresponding to the polypeptide of interest as a cDNA. For antisense suppression, the transcription factor or homologue cDNA is arranged in reverse orientation (with respect to the coding sequence) relative to the promoter sequence in the expression vector. The introduced sequence need not be the full length cDNA or gene, and need not be identical to the cDNA or gene found in the plant type to be transformed. Typically, the antisense sequence need only be capable of hybridizing to the target gene or RNA of interest. Thus, where the introduced sequence is of shorter length, a higher degree of homology to the endogenous transcription factor sequence will be needed for effective antisense suppression. While antisense sequences of various lengths can be utilized, preferably,

the introduced antisense sequence in the vector will be at least 30 nucleotides in length, and improved antisense suppression will typically be observed as the length of the antisense sequence increases. Preferably, the length of the antisense sequence in the vector will be greater than 100 nucleotides. Transcription of an antisense construct as described results in the production of

5 RNA molecules that are the reverse complement of mRNA molecules transcribed from the endogenous transcription factor gene in the plant cell.

Suppression of endogenous transcription factor gene expression can also be achieved using a ribozyme. Ribozymes are RNA molecules that possess highly specific endoribonuclease activity. The production and use of ribozymes are disclosed in U.S. Patent No.

10 4,987,071 and U.S. Patent No. 5,543,508. Synthetic ribozyme sequences including antisense RNAs can be used to confer RNA cleaving activity on the antisense RNA, such that endogenous mRNA molecules that hybridize to the antisense RNA are cleaved, which in turn leads to an enhanced antisense inhibition of endogenous gene expression.

Vectors in which RNA encoded by a transcription factor or transcription factor

15 homologue cDNA is over-expressed can also be used to obtain co-suppression of a corresponding endogenous gene, e.g., in the manner described in U.S. Patent No. 5,231,020 to Jorgensen. Such co-suppression (also termed sense suppression) does not require that the entire transcription factor cDNA be introduced into the plant cells, nor does it require that the introduced sequence be exactly identical to the endogenous transcription factor gene of interest. However, as with

20 antisense suppression, the suppressive efficiency will be enhanced as specificity of hybridization is increased, e.g., as the introduced sequence is lengthened, and/or as the sequence similarity between the introduced sequence and the endogenous transcription factor gene is increased.

Vectors expressing an untranslatable form of the transcription factor mRNA, e.g., sequences comprising one or more stop codon, or nonsense mutation) can also be used to

25 suppress expression of an endogenous transcription factor, thereby reducing or eliminating its activity and modifying one or more traits. Methods for producing such constructs are described in U.S. Patent No. 5,583,021. Preferably, such constructs are made by introducing a premature stop codon into the transcription factor gene. Alternatively, a plant trait can be modified by gene silencing using double-strand RNA (Sharp (1999) Genes and Development 13: 139-141).

30 Another method for abolishing the expression of a gene is by insertion mutagenesis using the T-DNA of *Agrobacterium tumefaciens*. After generating the insertion mutants, the mutants can be screened to identify those containing the insertion in a transcription factor or transcription factor homologue gene. Plants containing a single transgene insertion

event at the desired gene can be crossed to generate homozygous plants for the mutation (Koncz et al. (1992) Methods in Arabidopsis Research, World Scientific).

Alternatively, a plant phenotype can be altered by eliminating an endogenous gene, such as a transcription factor or transcription factor homologue, e.g., by homologous recombination (Kempin et al. (1997) Nature 389:802).

A plant trait can also be modified by using the cre-lox system (for example, as described in US Pat. No. 5,658,772). A plant genome can be modified to include first and second lox sites that are then contacted with a Cre recombinase. If the lox sites are in the same orientation, the intervening DNA sequence between the two sites is excised. If the lox sites are in the opposite orientation, the intervening sequence is inverted.

The polynucleotides and polypeptides of this invention can also be expressed in a plant in the absence of an expression cassette by manipulating the activity or expression level of the endogenous gene by other means. For example, by ectopically expressing a gene by T-DNA activation tagging (Ichikawa et al. (1997) Nature 390 698-701; Kakimoto et al. (1996) Science 274: 982-985). This method entails transforming a plant with a gene tag containing multiple transcriptional enhancers and once the tag has inserted into the genome, expression of a flanking gene coding sequence becomes deregulated. In another example, the transcriptional machinery in a plant can be modified so as to increase transcription levels of a polynucleotide of the invention (See, e.g., PCT Publications WO 96/06166 and WO 98/53057 which describe the modification of the DNA binding specificity of zinc finger proteins by changing particular amino acids in the DNA binding motif).

The transgenic plant can also include the machinery necessary for expressing or altering the activity of a polypeptide encoded by an endogenous gene, for example by altering the phosphorylation state of the polypeptide to maintain it in an activated state.

Transgenic plants (or plant cells, or plant explants, or plant tissues) incorporating the polynucleotides of the invention and/or expressing the polypeptides of the invention can be produced by a variety of well established techniques as described above. Following construction of a vector, most typically an expression cassette, including a polynucleotide, e.g., encoding a transcription factor or transcription factor homologue, of the invention, standard techniques can be used to introduce the polynucleotide into a plant, a plant cell, a plant explant or a plant tissue of interest. Optionally, the plant cell, explant or tissue can be regenerated to produce a transgenic plant.

The plant can be any higher plant, including gymnosperms, monocotyledonous and dicotyledonous plants. Suitable protocols are available for *Leguminosae* (alfalfa, soybean,

clover, etc.), *Umbelliferae* (carrot, celery, parsnip), *Cruciferae* (cabbage, radish, rapeseed, broccoli, etc.), *Curcubitaceae* (melons and cucumber), *Gramineae* (wheat, corn, rice, barley, millet, etc.), *Solanaceae* (potato, tomato, tobacco, peppers, etc.), and various other crops. See protocols described in Ammirato et al. (1984) Handbook of Plant Cell Culture –Crop Species.

- 5 Macmillan Publ. Co. Shimamoto et al. (1989) Nature 338:274-276; Fromm et al. (1990) Bio/Technology 8:833-839; and Vasil et al. (1990) Bio/Technology 8:429-434.

Transformation and regeneration of both monocotyledonous and dicotyledonous plant cells is now routine, and the selection of the most appropriate transformation technique will be determined by the practitioner. The choice of method will vary with the type of plant to be transformed; those skilled in the art will recognize the suitability of particular methods for given plant types. Suitable methods can include, but are not limited to: electroporation of plant protoplasts; liposome-mediated transformation; polyethylene glycol (PEG) mediated transformation; transformation using viruses; micro-injection of plant cells; micro-projectile bombardment of plant cells; vacuum infiltration; and *Agrobacterium tumefaciens* mediated transformation. Transformation means introducing a nucleotide sequence in a plant in a manner to cause stable or transient expression of the sequence.

Successful examples of the modification of plant characteristics by transformation with cloned sequences which serve to illustrate the current knowledge in this field of technology, and which are herein incorporated by reference, include: U.S. Patent Nos. 5,571,706; 5,677,175; 5,510,471; 5,750,386; 5,597,945; 5,589,615; 5,750,871; 5,268,526; 5,780,708; 5,538,880; 5,773,269; 5,736,369 and 5,610,042.

Following transformation, plants are preferably selected using a dominant selectable marker incorporated into the transformation vector. Typically, such a marker will confer antibiotic or herbicide resistance on the transformed plants, and selection of transformants can be accomplished by exposing the plants to appropriate concentrations of the antibiotic or herbicide.

After transformed plants are selected and grown to maturity, those plants showing a modified trait are identified. The modified trait can be any of those traits described above. Additionally, to confirm that the modified trait is due to changes in expression levels or activity of the polypeptide or polynucleotide of the invention can be determined by analyzing mRNA expression using Northern blots, RT-PCR or microarrays, or protein expression using immunoblots or Western blots or gel shift assays.

INTEGRATED SYSTEMS—SEQUENCE IDENTITY

Additionally, the present invention may be an integrated system, computer or computer readable medium that comprises an instruction set for determining the identity of one or more sequences in a database. In addition, the instruction set can be used to generate or identify
5 sequences that meet any specified criteria. Furthermore, the instruction set may be used to associate or link certain functional benefits, such modified structure and development characteristics, with one or more identified sequence.

For example, the instruction set can include, e.g., a sequence comparison or other alignment program, e.g., an available program such as, for example, the Wisconsin Package
10 Version 10.0, such as BLAST, FASTA, PILEUP, FINDPATTERNS or the like (GCG, Madison, WI). Public sequence databases such as GenBank, EMBL, Swiss-Prot and PIR or private sequence databases such as PhytoSeq (Incyte Pharmaceuticals, Palo Alto, CA) can be searched.

Alignment of sequences for comparison can be conducted by the local homology algorithm of Smith and Waterman (1981) Adv. Appl. Math. 2:482, by the homology alignment
15 algorithm of Needleman and Wunsch (1970) J. Mol. Biol. 48:443, by the search for similarity method of Pearson and Lipman (1988) Proc. Natl. Acad. Sci. U.S.A. 85: 2444, by computerized implementations of these algorithms. After alignment, sequence comparisons between two (or more) polynucleotides or polypeptides are typically performed by comparing sequences of the two sequences over a comparison window to identify and compare local regions of sequence
20 similarity. The comparison window can be a segment of at least about 20 contiguous positions, usually about 50 to about 200, more usually about 100 to about 150 contiguous positions. A description of the method is provided in Ausubel et al., *supra*.

A variety of methods of determining sequence relationships can be used, including manual alignment and computer assisted sequence alignment and analysis. This later
25 approach is a preferred approach in the present invention, due to the increased throughput afforded by computer assisted methods. As noted above, a variety of computer programs for performing sequence alignment are available, or can be produced by one of skill.

One example algorithm that is suitable for determining percent sequence identity and sequence similarity is the BLAST algorithm, which is described in Altschul et al. J. Mol. Biol.
30 215:403-410 (1990). Software for performing BLAST analyses is publicly available, e.g., through the National Center for Biotechnology Information (<http://www.ncbi.nlm.nih.gov/>). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is

referred to as the neighborhood word score threshold (Altschul et al., *supra*). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are then extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for

5 nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of

10 one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, a cutoff of 100, M=5, N=-4, and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength (W) of 3, an expectation (E)

15 of 10, and the BLOSUM62 scoring matrix (*see* Henikoff & Henikoff (1989) Proc. Natl. Acad. Sci. USA 89:10915).

In addition to calculating percent sequence identity, the BLAST algorithm also performs a statistical analysis of the similarity between two sequences (*see*, e.g., Karlin & Altschul (1993) Proc. Natl. Acad. Sci. USA 90:5873-5787). One measure of similarity provided

20 by the BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For example, a nucleic acid is considered similar to a reference sequence (and, therefore, in this context, homologous) if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.1, or less than about 0.01, and or

25 even less than about 0.001. An additional example of a useful sequence alignment algorithm is PILEUP. PILEUP creates a multiple sequence alignment from a group of related sequences using progressive, pairwise alignments. The program can align, e.g., up to 300 sequences of a maximum length of 5,000 letters.

The integrated system, or computer typically includes a user input interface

30 allowing a user to selectively view one or more sequence records corresponding to the one or more character strings, as well as an instruction set which aligns the one or more character strings with each other or with an additional character string to identify one or more region of sequence similarity. The system may include a link of one or more character strings with a particular

phenotype or gene function. Typically, the system includes a user readable output element which displays an alignment produced by the alignment instruction set.

The methods of this invention can be implemented in a localized or distributed computing environment. In a distributed environment, the methods may implemented on a single computer comprising multiple processors or on a multiplicity of computers. The computers can be linked, e.g. through a common bus, but more preferably the computer(s) are nodes on a network. The network can be a generalized or a dedicated local or wide-area network and, in certain preferred embodiments, the computers may be components of an intra-net or an internet.

Thus, the invention provides methods for identifying a sequence similar or homologous to one or more polynucleotides as noted herein, or one or more target polypeptides encoded by the polynucleotides, or otherwise noted herein and may include linking or associating a given plant phenotype or gene function with a sequence. In the methods, a sequence database is provided (locally or across an inter or intra net) and a query is made against the sequence database using the relevant sequences herein and associated plant phenotypes or gene functions.

Any sequence herein can be entered into the database, before or after querying the database. This provides for both expansion of the database and, if done before the querying step, for insertion of control sequences into the database. The control sequences can be detected by the query to ensure the general integrity of both the database and the query. As noted, the query can be performed using a web browser based interface. For example, the database can be a centralized public database such as those noted herein, and the querying can be done from a remote terminal or computer across an internet or intranet.

EXAMPLES

The following examples are intended to illustrate but not limit the present invention.

25 EXAMPLE I. FULL LENGTH GENE IDENTIFICATION AND CLONING

Putative transcription factor sequences (genomic or ESTs) related to known transcription factors were identified in the *Arabidopsis thaliana* GenBank database using the tblastn sequence analysis program using default parameters and a P-value cutoff threshold of -4 or -5 or lower, depending on the length of the query sequence. Putative transcription factor sequence hits were then screened to identify those containing particular sequence strings. If the sequence hits contained such sequence strings, the sequences were confirmed as transcription factors.

Alternatively, *Arabidopsis thaliana* cDNA libraries derived from different tissues or treatments, or genomic libraries were screened to identify novel members of a transcription family using a low stringency hybridization approach. Probes were synthesized using gene specific primers in a standard PCR reaction (annealing temperature 60° C) and labeled with ³²P dCTP using the High Prime DNA Labeling Kit (Boehringer Mannheim). Purified radiolabelled probes were added to filters immersed in Church hybridization medium (0.5 M NaPO₄ pH 7.0, 7% SDS, 1 % w/v bovine serum albumin) and hybridized overnight at 60 °C with shaking. Filters were washed two times for 45 to 60 minutes with 1xSSC, 1% SDS at 60° C.

To identify additional sequence 5' or 3' of a partial cDNA sequence in a cDNA library, 5' and 3' rapid amplification of cDNA ends (RACE) was performed using the Marathon™ cDNA amplification kit (Clontech, Palo Alto, CA). Generally, the method entailed first isolating poly(A) mRNA, performing first and second strand cDNA synthesis to generate double stranded cDNA, blunting cDNA ends, followed by ligation of the Marathon™ Adaptor to the cDNA to form a library of adaptor-ligated ds cDNA.

Gene-specific primers were designed to be used along with adaptor specific primers for both 5' and 3' RACE reactions. Nested primers, rather than single primers, were used to increase PCR specificity. Using 5' and 3' RACE reactions, 5' and 3' RACE fragments were obtained, sequenced and cloned. The process can be repeated until 5' and 3' ends of the full-length gene were identified. Then the full-length cDNA was generated by PCR using primers specific to 5' and 3' ends of the gene by end-to-end PCR.

EXAMPLE II. CONSTRUCTION OF EXPRESSION VECTORS

The sequence was amplified from a genomic or cDNA library using primers specific to sequences upstream and downstream of the coding region. The expression vector was pMEN20 or pMEN65, which are both derived from pMON316 (Sanders et al, (1987) Nucleic Acids Research 15:1543-58) and contain the CaMV 35S promoter to express transgenes. To clone the sequence into the vector, both pMEN20 and the amplified DNA fragment were digested separately with SalI and NotI restriction enzymes at 37° C for 2 hours. The digestion products were subject to electrophoresis in a 0.8% agarose gel and visualized by ethidium bromide staining. The DNA fragments containing the sequence and the linearized plasmid were excised and purified by using a Qiaquick gel extraction kit (Qiagen, CA). The fragments of interest were ligated at a ratio of 3:1 (vector to insert). Ligation reactions using T4 DNA ligase (New England Biolabs, MA) were carried out at 16° C for 16 hours. The ligated DNAs were transformed into

competent cells of the *E. coli* strain DH5alpha by using the heat shock method. The transformations were plated on LB plates containing 50 mg/l kanamycin (Sigma).

Individual colonies were grown overnight in five milliliters of LB broth containing 50 mg/l kanamycin at 37° C. Plasmid DNA was purified by using Qiaquick Mini
5 Prep kits (Qiagen, CA).

EXAMPLE III. TRANSFORMATION OF *AGROBACTERIUM* WITH THE EXPRESSION VECTOR

After the plasmid vector containing the gene was constructed, the vector was used to transform *Agrobacterium tumefaciens* cells expressing the gene products. The stock of
10 *Agrobacterium tumefaciens* cells for transformation were made as described by Nagel et al. (1990) FEMS Microbiol Letts. 67: 325-328. *Agrobacterium* strain ABI was grown in 250 ml LB medium (Sigma) overnight at 28°C with shaking until an absorbance (A_{600}) of 0.5 – 1.0 was reached. Cells were harvested by centrifugation at 4,000 x g for 15 min at 4° C. Cells were then resuspended in 250 µl chilled buffer (1 mM HEPES, pH adjusted to 7.0 with KOH). Cells were
15 centrifuged again as described above and resuspended in 125 µl chilled buffer. Cells were then centrifuged and resuspended two more times in the same HEPES buffer as described above at a volume of 100 µl and 750 µl, respectively. Resuspended cells were then distributed into 40 µl aliquots, quickly frozen in liquid nitrogen, and stored at -80° C.

Agrobacterium cells were transformed with plasmids prepared as described
20 above following the protocol described by Nagel et al. For each DNA construct to be transformed, 50 – 100 ng DNA (generally resuspended in 10 mM Tris-HCl, 1 mM EDTA, pH 8.0) was mixed with 40 µl of *Agrobacterium* cells. The DNA/cell mixture was then transferred to a chilled cuvette with a 2mm electrode gap and subject to a 2.5 kV charge dissipated at 25 µF and 200 µF using a Gene Pulser II apparatus (Bio-Rad). After electroporation, cells were
25 immediately resuspended in 1.0 ml LB and allowed to recover without antibiotic selection for 2 – 4 hours at 28° C in a shaking incubator. After recovery, cells were plated onto selective medium of LB broth containing 100 µg/ml spectinomycin (Sigma) and incubated for 24-48 hours at 28° C. Single colonies were then picked and inoculated in fresh medium. The presence of the plasmid construct was verified by PCR amplification and sequence analysis.

30 EXAMPLE IV. TRANSFORMATION OF *ARABIDOPSIS* PLANTS WITH *AGROBACTERIUM TUMEFACIENS* WITH EXPRESSION VECTOR

After transformation of *Agrobacterium tumefaciens* with plasmid vectors containing the gene, single *Agrobacterium* colonies were identified, propagated, and used to

transform *Arabidopsis* plants. Briefly, 500 ml cultures of LB medium containing 50 mg/l kanamycin were inoculated with the colonies and grown at 28°C with shaking for 2 days until an absorbance (A_{600}) of > 2.0 is reached. Cells were then harvested by centrifugation at 4,000 x g for 10 min, and resuspended in infiltration medium (1/2 X Murashige and Skoog salts (Sigma), 1
5 X Gamborg's B-5 vitamins (Sigma), 5.0% (w/v) sucrose (Sigma), 0.044 μ M benzylamino purine (Sigma), 200 μ L Silwet L-77 (Lehle Seeds) until an absorbance (A_{600}) of 0.8 was reached.

Prior to transformation, *Arabidopsis thaliana* seeds (ecotype Columbia) were sown at a density of ~10 plants per 4" pot onto Pro-Mix BX potting medium (Hummert International) covered with fiberglass mesh (18 mm X 16 mm). Plants were grown under
10 continuous illumination (50-75 μ E/m²/sec) at 22-23°C with 65-70% relative humidity. After about 4 weeks, primary inflorescence stems (bolts) are cut off to encourage growth of multiple secondary bolts. After flowering of the mature secondary bolts, plants were prepared for transformation by removal of all siliques and opened flowers.

The pots were then immersed upside down in the mixture of *Agrobacterium*
15 infiltration medium as described above for 30 sec, and placed on their sides to allow draining into a 1' x 2' flat surface covered with plastic wrap. After 24 h, the plastic wrap was removed and pots are turned upright. The immersion procedure was repeated one week later, for a total of two immersions per pot. Seeds were then collected from each transformation pot and analyzed following the protocol described below.

20 EXAMPLE V. IDENTIFICATION OF ARABIDOPSIS PRIMARY TRANSFORMANTS

Seeds collected from the transformation pots were sterilized essentially as follows. Seeds were dispersed into in a solution containing 0.1% (v/v) Triton X-100 (Sigma) and sterile H₂O and washed by shaking the suspension for 20 min. The wash solution was then drained and replaced with fresh wash solution to wash the seeds for 20 min with shaking. After
25 removal of the second wash solution, a solution containing 0.1% (v/v) Triton X-100 and 70% ethanol (Equistar) was added to the seeds and the suspension was shaken for 5 min. After removal of the ethanol/detergent solution, a solution containing 0.1% (v/v) Triton X-100 and 30% (v/v) bleach (Clorox) was added to the seeds, and the suspension was shaken for 10 min. After
30 removal of the bleach/detergent solution, seeds were then washed five times in sterile distilled H₂O. The seeds were stored in the last wash water at 4°C for 2 days in the dark before being plated onto antibiotic selection medium (1 X Murashige and Skoog salts (pH adjusted to 5.7 with 1M KOH), 1 X Gamborg's B-5 vitamins, 0.9% phytagar (Life Technologies), and 50 mg/l kanamycin). Seeds were germinated under continuous illumination (50-75 μ E/m²/sec) at 22-23°C

C. After 7-10 days of growth under these conditions, kanamycin resistant primary transformants (T_1 generation) were visible and obtained. These seedlings were transferred first to fresh selection plates where the seedlings continued to grow for 3-5 more days, and then to soil (Pro-Mix BX potting medium).

Primary transformants were crossed and progeny seeds (T_2) collected; kanamycin resistant seedlings were selected and analyzed. The expression levels of the recombinant polynucleotides in the transformants varies from about a 5% expression level increase to a least a 100% expression level increase. Similar observations are made with respect to polypeptide level expression.

EXAMPLE VI. IDENTIFICATION OF ARABIDOPSIS PLANTS WITH TRANSCRIPTION FACTOR GENE KNOCKOUTS

The screening of insertion mutagenized *Arabidopsis* collections for null mutants in a known target gene was essentially as described in Krysan et al (1999) Plant Cell 11:2283-2290. Briefly, gene-specific primers, nested by 5-250 pb to each others, were designed from the 5' and 3' regions of a known target gene. Similarly, nested sets of primers were also created specific to each of the T-DNA or transposon ends (the "right" and "left" borders). All possible combinations of gene specific and T-DNA/transposon primers were used to detect by PCR an insertion event within or close to the target gene. The amplified DNA fragments were then sequenced which allows the precise determination of the T-DNA/transposon insertion point relative to the target gene. Insertion events within the coding or intervening sequence of the genes were deconvoluted from a pool comprising a plurality of insertion events to a single unique mutant plant for functional characterization. The method is described in more detail in Yu and Adam, US Application Serial No. 09/177,733 filed October 23, 1998.

EXAMPLE VII. IDENTIFICATION OF STRUCTURE AND DEVELOPMENT CHARACTERISTICS PHENOTYPE IN OVEREXPRESSOR OR GENE KNOCKOUT PLANTS

Experiments were performed to identify those transformants or knockouts that exhibited a modified structure and development characteristics. For such studies, the transformants were observed by eye to identify novel structural or developmental characteristics associated with the ectopic expression of the polynucleotides or polypeptides of the invention.

Table 3 shows the phenotypes observed for particular overexpressor or knockout plants and provides the SEQ ID No., the internal reference code (GID), whether a knockout or overexpressor plant was analyzed and the observed phenotype.

Table 3

SEQ ID No.	GID	Knockout (KO) or overexpressor (OE)	Phenotype observed
1	G727	OE	Plants were small, and more dark green in color, late flowering and poorly fertile.
3	G732	OE	Plants were small and inflorescence was unelongated. Flowers parts appeared to be unelongated and the plants were semi-sterile.
5	G9	OE	Increased root mass
7	G428	OE	Lobed and highly serrated leaves and abnormal first and second whorl floral organs
9	G869	OE	Undeveloped or small anthers
11	G1269	OE	Extended petioles and leaves pointed upwards
13	G1038	OE	Altered leaf shape
15	G438	KO	Reduced lignin in stem
17	G571	KO	Delayed senescence at the end of the plant lifecycle
19	G748	OE	More vascular bundles in stem
21	G431	OE	Severe developmental abnormalities such as altered branching, twisted rosette leaves, flowers with missing pistils, fused stamens and atypical numbers of petals and stamens, reduced secondary bolts, and lack of cauline leaves.
23	G187	OE	Plants had long, thin cotyledons and reduced apical dominance. Several flower abnormalities, including underdeveloped, sepaloid petals and underdeveloped anthers were also observed.
25	G470	OE	Plants were sterile due to failure of anthers to elongate
27	G615	OE	Plants were sterile due to failure of anthers to develop and failure of stamens to elongate. Fused cotyledons and absence of a shoot apical meristem and true leaves was also observed.
29	G1073	OE	Increased plant size and serrated leaves

For a particular overexpressor that shows a less beneficial structure and development characteristic, it may be more useful to select a plant with a decreased expression of the particular transcription factor. For a particular knockout that shows a less beneficial structure and development characteristic, it may be more useful to select a plant with an increased expression of the particular transcription factor.

EXAMPLE VIII. IDENTIFICATION OF HOMOLOGOUS SEQUENCES

Homologous sequences from *Arabidopsis* and plant species other than *Arabidopsis* were identified using database sequence search tools, such as the Basic Local Alignment Search Tool (BLAST) (Altschul et al. (1990) J. Mol. Biol. 215:403-410; and Altschul et al. (1997) Nucl. Acid Res. 25: 3389-3402). The tblastx sequence analysis programs were employed using the BLOSUM-62 scoring matrix (Henikoff, S. and Henikoff, J. G. (1992) Proc. Natl. Acad. Sci. USA 89: 10915-10919).

Identified *Arabidopsis* homologous sequences are provided in Figure 2 and included in the Sequence Listing. The percent sequence identity among these sequences is as low as 47% sequence identity. Additionally, the entire NCBI GenBank database was filtered for sequences from all plants except *Arabidopsis thaliana* by selecting all entries in the NCBI GenBank database associated with NCBI taxonomic ID 33090 (Viridiplantae; all plants) and excluding entries associated with taxonomic ID 3701 (*Arabidopsis thaliana*). These sequences were compared to sequences representing genes of SEQ IDs Nos. 1-54 on 9/26/2000 using the Washington University TBLASTX algorithm (version 2.0a19MP). For each gene of SEQ IDs Nos. 1-54, individual comparisons were ordered by probability score (P-value), where the score reflects the probability that a particular alignment occurred by chance. For example, a score of $3.6e-40$ is 3.6×10^{-40} . For up to ten species, the gene with the lowest P-value (and therefore the most likely homolog) is listed in Figure 3.

In addition to P-values, comparisons were also scored by percentage identity. Percentage identity reflects the degree to which two segments of DNA or protein are identical over a particular length. The ranges of percent identity between the non-*Arabidopsis* genes shown in Figure 3 and the *Arabidopsis* genes in the sequence listing are: SEQ ID No. 1: 36%-69%; SEQ ID No. 3: 46%-54%; SEQ ID No. 5: 57%-72%; SEQ ID No. 7: 54%-69%; SEQ ID No. 9: 31%-68%; SEQ ID No. 11: 47%-90%; SEQ ID No. 13: 34%-82%; SEQ ID No. 15: 49%-88%; SEQ ID No. 17: 56%-67%; SEQ ID No. 19: 39%-61%; SEQ ID No. 21: 61%-87%; SEQ ID No. 23: 38%-85%; SEQ ID No. 25: 44%-94%; SEQ ID No. 27: 35%-44%; SEQ ID No. 29: 37%-71%; SEQ ID No. 31: 38%-77%; SEQ ID No. 33: 57%-69%; SEQ ID No. 35: 54%-69%; SEQ ID No. 37: 60%-75%; SEQ ID No. 39: 47%-65%; SEQ ID No. 41: 60%-88%; SEQ ID No. 43: 43%-87%; and SEQ ID No. 45: 53%-97%.

The polynucleotides and polypeptides in the Sequence Listing and the identified homologous sequences may be stored in a computer system and have associated or linked with the sequences a function, such as that the polynucleotides and polypeptides are useful for modifying the structure and development characteristics of a plant.

All references, publications, patents and other documents herein are incorporated by reference in their entirety for all purposes. Although the invention has been described with reference to the embodiments and examples above, it should be understood that various
5 modifications can be made without departing from the spirit of the invention.

What is claimed is:

1. A transgenic plant with modified structure and development characteristics, which plant comprises a recombinant polynucleotide comprising a nucleotide sequence selected from the group consisting of:
 - 5 (a) a nucleotide sequence encoding a polypeptide comprising a sequence selected from SEQ ID Nos. 2N, where N=1-23, or a complementary nucleotide sequence thereof;
 - (b) a nucleotide sequence encoding a polypeptide comprising a conservatively substituted variant of a polypeptide of (a);
 - (c) a nucleotide sequence comprising a sequence selected from those of SEQ ID Nos. 2N-
10 1, where N=1-23, or a complementary nucleotide sequence thereof;
 - (d) a nucleotide sequence comprising silent substitutions in a nucleotide sequence of (c);
 - (e) a nucleotide sequence which hybridizes under stringent conditions to a nucleotide sequence of one or more of: (a), (b), (c), or (d);
 - (f) a nucleotide sequence comprising at least 15 consecutive nucleotides of a sequence of
15 any of (a)-(e);
 - (g) a nucleotide sequence comprising a subsequence or fragment of any of (a)-(f), which subsequence or fragment encodes a polypeptide that modifies a plant's structure and development characteristics;
 - (h) a nucleotide sequence having at least 31% sequence identity to a nucleotide sequence
20 of any of (a)-(g);
 - (i) a nucleotide sequence having at least 60% identity sequence identity to a nucleotide sequence of any of (a)-(g);
 - (j) a nucleotide sequence which encodes a polypeptide having at least 31% identity sequence identity to a polypeptide of SEQ ID Nos. 2N, where N=1-23;
 - 25 (k) a nucleotide sequence which encodes a polypeptide having at least 60% identity sequence identity to a polypeptide of SEQ ID Nos. 2N, where N=1-23; and
 - (l) a nucleotide sequence which encodes a polypeptide having at least 65% sequence identity to a conserved domain of a polypeptide of SEQ ID Nos. 2N, where N=1-23.
- 30 2. The transgenic plant of claim 1, further comprising a constitutive, inducible, or tissue-active promoter operably linked to said nucleotide sequence.
3. The transgenic plant of claim 1, wherein the plant is selected from the group consisting of: soybean, wheat, corn, potato, cotton, rice, oilseed rape, sunflower, alfalfa, sugarcane, turf,

banana, blackberry, blueberry, strawberry, raspberry, cantaloupe, carrot, cauliflower, coffee, cucumber, eggplant, grapes, honeydew, lettuce, mango, melon, onion, papaya, peas, peppers, pineapple, spinach, squash, sweet corn, tobacco, tomato, watermelon, rosaceous fruits, and vegetable brassicas.

5

4. An isolated or recombinant polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) a nucleotide sequence encoding a polypeptide comprising a sequence selected from SEQ ID Nos. 2N, where N=1-23, or a complementary nucleotide sequence thereof;
- 10 (b) a nucleotide sequence encoding a polypeptide comprising a conservatively substituted variant of a polypeptide of (a);
- (c) a nucleotide sequence comprising a sequence selected from those of SEQ ID Nos. 2N-1, where N=1-23, or a complementary nucleotide sequence thereof;
- (d) a nucleotide sequence comprising silent substitutions in a nucleotide sequence of (c);
- 15 (e) a nucleotide sequence which hybridizes under stringent conditions to a nucleotide sequence of one or more of: (a), (b), (c), or (d);
- (f) a nucleotide sequence comprising at least 15 consecutive nucleotides of a sequence of any of (a)-(e);
- (g) a nucleotide sequence comprising a subsequence or fragment of any of (a)-(f), which
20 subsequence or fragment encodes a polypeptide that modifies a plant's structure and development characteristics;
- (h) a nucleotide sequence having at least 31% sequence identity to a nucleotide sequence of any of (a)-(g);
- (i) a nucleotide sequence having at least 60% identity sequence identity to a nucleotide
25 sequence of any of (a)-(g);
- (j) a nucleotide sequence which encodes a polypeptide having at least 31% identity sequence identity to a polypeptide of SEQ ID Nos. 2N, where N=1-23;
- (k) a nucleotide sequence which encodes a polypeptide having at least 60% identity sequence identity to a polypeptide of SEQ ID Nos. 2N, where N=1-23; and
- 30 (l) a nucleotide sequence which encodes a conserved domain of a polypeptide having at least 65% sequence identity to a conserved domain of a polypeptide of SEQ ID Nos. 2N, where N=1-23.

5. The isolated or recombinant polynucleotide of claim 4, further comprising a constitutive, inducible, or tissue-active promoter operably linked to the nucleotide sequence.
6. A cloning or expression vector comprising the isolated or recombinant polynucleotide of claim 4.
7. A cell comprising the cloning or expression vector of claim 6.
8. A transgenic plant comprising the isolated or recombinant polynucleotide of claim 4.
9. A composition produced by one or more of:
- (a) incubating one or more polynucleotide of claim 4 with a nuclease;
 - (b) incubating one or more polynucleotide of claim 4 with a restriction enzyme;
 - (c) incubating one or more polynucleotide of claim 4 with a polymerase;
 - (d) incubating one or more polynucleotide of claim 4 with a polymerase and a primer;
 - (e) incubating one or more polynucleotide of claim 4 with a cloning vector, or
 - (f) incubating one or more polynucleotide of claim 4 with a cell.
10. A composition comprising two or more different polynucleotides of claim 4.
11. An isolated or recombinant polypeptide comprising a subsequence of at least about 15 contiguous amino acids encoded by the recombinant or isolated polynucleotide of claim 4.
12. A plant ectopically expressing an isolated polypeptide of claim 11.
13. A method for producing a plant having a modified structure and development characteristic, the method comprising altering the expression of the isolated or recombinant polynucleotide of claim 4 or the expression levels or activity of a polypeptide of claim 11 in a plant, thereby producing a modified plant, and selecting the modified plant for modified structure and development characteristics thereby providing the modified plant with a modified structure and development characteristics.
14. The method of claim 13, wherein the polynucleotide is a polynucleotide of claim 4.

15. A method of identifying a factor that is modulated by or interacts with a polypeptide encoded by a polynucleotide of claim 4, the method comprising:
- (a) expressing a polypeptide encoded by the polynucleotide in a plant; and
 - (b) identifying at least one factor that is modulated by or interacts with the polypeptide.
- 5
16. The method of claim 15, wherein the identifying is performed by detecting binding by the polypeptide to a promoter sequence, or detecting interactions between an additional protein and the polypeptide in a yeast two hybrid system.
- 10 17. The method of claim 15, wherein the identifying is performed by detecting expression of a factor by hybridization to a microarray, subtractive hybridization or differential display.
18. A method of identifying a molecule that modulates activity or expression of a polynucleotide or polypeptide of interest, the method comprising:
- 15 (a) placing the molecule in contact with a plant comprising the polynucleotide or polypeptide encoded by the polynucleotide of claim 4; and,
- (b) monitoring one or more of:
- (i) expression level of the polynucleotide in the plant;
 - (ii) expression level of the polypeptide in the plant;
 - 20 (iii) modulation of an activity of the polypeptide in the plant; or
 - (iv) modulation of an activity of the polynucleotide in the plant.
19. An integrated system, computer or computer readable medium comprising one or more character strings corresponding to a polynucleotide of claim 4, or to a polypeptide encoded by the
- 25 polynucleotide.
20. The integrated system, computer or computer readable medium of claim 19, further comprising a link between said one or more sequence strings to a modified plant structure and development characteristics phenotype.
- 30
21. A method of identifying a sequence similar or homologous to one or more polynucleotides of claim 4, or one or more polypeptides encoded by the polynucleotides, the method comprising:
- (a) providing a sequence database; and,

(b) querying the sequence database with one or more target sequences corresponding to the one or more polynucleotides or to the one or more polypeptides to identify one or more sequence members of the database that display sequence similarity or homology to one or more of the one or more target sequences.

5

22. The method of claim 21, wherein the querying comprises aligning one or more of the target sequences with one or more of the one or more sequence members in the sequence database.

10 23. The method of claim 21, wherein the querying comprises identifying one or more of the one or more sequence members of the database that meet a user-selected identity criteria with one or more of the target sequences.

15 24. The method of claim 21, further comprising linking the one or more of the polynucleotides of claim 4, or encoded polypeptides, to a modified plant structure and development characteristics phenotype.

20 25. A plant comprising altered expression levels of an isolated or recombinant polynucleotide of claim 4.

20

26. A plant comprising altered expression levels or the activity of an isolated or recombinant polypeptide of claim 11.

25 27. A plant lacking a nucleotide sequence encoding a polypeptide of claim 11.

25

Figure 1

SEQ ID No.	GID	cDNA or protein	conserved domain
1	G727	cDNA	
2	G727	protein	226-269
3	G732	cDNA	
4	G732	protein	31-9
5	G9	cDNA	
6	G9	protein	62-127
7	G428	cDNA	
8	G428	protein	229-292
9	G869	cDNA	
10	G869	protein	109-177
11	G1269	cDNA	
12	G1269	protein	27-83
13	G1038	cDNA	
14	G1038	protein	198-247
15	G438	cDNA	
16	G438	protein	22-85
17	G571	cDNA	
18	G571	protein	160-220
19	G748	cDNA	
20	G748	protein	112-140
21	G431	cDNA	
22	G431	protein	286-335
23	G187	cDNA	
24	G187	protein	172-228
25	G470	cDNA	
26	G470	protein	61-393
27	G615	cDNA	
28	G615	protein	88-147
29	G1073	cDNA	
30	G1073	protein	33-42, 78-175

Figure 2

SEQ ID No.	GID	homolog	cDNA or protein	conserved domain
31	G1493	homolog of G727	cDNA	
32	G1493	homolog of G727	protein	242-289
33	G993	homolog of G9	cDNA	
34	G993	homolog of G9	protein	69-134
35	G867	homolog of G9	cDNA	
36	G867	homolog of G9	protein	59-124
37	G1930	homolog of G9	cDNA	
38	G1930	homolog of G9	protein	59-124
39	G1594	homolog of G428	cDNA	
40	G1594	homolog of G428	protein	262-325
41	G391	homolog of G438	cDNA	
42	G391	homolog of G438	protein	25-85
43	G390	homolog of G438	cDNA	
44	G390	homolog of G438	protein	18-81
45	G1548	homolog of G438	cDNA	
46	G1548	homolog of G438	protein	17-77

Figure 3A

SEQ ID No.	GID	Genbank NID	P-value	Species
1	G727	7283684	2.20E-56	Glycine max
1	G727	7206180	8.40E-42	Medicago truncatula
1	G727	7614196	2.20E-40	Lotus japonicus
1	G727	572293	1.20E-31	Oryza sativa
1	G727	7218448	7.70E-30	Sorghum bicolor
1	G727	9291284	1.80E-27	Lycopersicon hirsutum
1	G727	8901641	5.10E-27	Hordeum vulgare
1	G727	8380453	6.60E-24	Gossypium arboreum
1	G727	9962201	2.10E-12	Cryptomeria japonica
1	G727	8122498	3.10E-08	Lycopersicon esculentum
3	G732	5048074	5.60E-30	Gossypium hirsutum
3	G732	4384142	6.10E-30	Lycopersicon esculentum
3	G732	7623218	6.10E-30	Gossypium arboreum
3	G732	4457220	1.80E-29	Capsicum chinense
3	G732	7284989	4.50E-28	Glycine max
3	G732	9650827	1.20E-27	Petroselinum crispum
3	G732	7205618	2.20E-26	Medicago truncatula
3	G732	3854258	1.40E-22	Populus tremula x Populus tremuloides
5	G9	7643366	6.80E-56	Medicago truncatula
5	G9	8669779	4.20E-50	Glycine max
5	G9	8329389	1.50E-48	Mesembryanthemum crystallinum
5	G9	9851335	3.50E-42	Sorghum bicolor
5	G9	7412012	1.50E-41	Lycopersicon esculentum
5	G9	10450225	1.30E-38	Solanum tuberosum
5	G9	8902194	8.30E-36	Hordeum vulgare
5	G9	7722547	2.60E-33	Lotus japonicus
5	G9	9696857	1.90E-32	Triticum aestivum
5	G9	7324245	2.40E-32	Lycopersicon pennellii
7	G428	3327268	5.50E-65	Ipomoea nil
7	G428	4589883	1.20E-60	Nicotiana tabacum
7	G428	1814233	2.20E-56	Solanum tuberosum
7	G428	7581978	8.50E-56	Dendrobium grex Madame Thong-In
7	G428	4098241	1.50E-53	Lycopersicon esculentum
7	G428	4099825	1.30E-38	Picea mariana
7	G428	3462611	2.50E-38	Pisum sativum
7	G428	3928842	1.90E-37	Picea abies
7	G428	9699343	2.70E-35	Triticum aestivum
7	G428	1008878	4.80E-35	Zea mays
9	G869	10235055	1.00E-19	Glycine max
9	G869	2213784	1.60E-19	Lycopersicon esculentum
9	G869	3065894	9.20E-19	Nicotiana tabacum
9	G869	8570080	5.30E-18	Oryza sativa
9	G869	7560260	1.90E-17	Medicago truncatula
9	G869	9850452	9.30E-16	Sorghum bicolor
9	G869	9963144	1.10E-13	Cryptomeria japonica
9	G869	9660634	1.90E-13	Secale cereale
9	G869	9362061	3.40E-13	Triticum aestivum
9	G869	7788764	7.20E-13	Lotus japonicus
11	G1269	9565366	7.00E-37	Glycine max
11	G1269	5272360	8.10E-37	Lycopersicon esculentum
11	G1269	9119112	8.40E-28	Medicago truncatula
11	G1269	9852711	2.10E-22	Sorghum bicolor

Figure 3B

SEQ ID No.	GID	Genbank NID	P-value	Species
11	G1269	9255178	1.10E-18	Zea mays
11	G1269	10447957	8.60E-15	Solanum tuberosum
11	G1269	9435251	1.20E-09	Hordeum vulgare
11	G1269	3858030	3.20E-09	Populus balsamifera subsp. trichocarpa
11	G1269	9696112	3.80E-09	Triticum aestivum
11	G1269	8213273	4.90E-09	Oryza sativa
13	G1038	8748344	8.00E-37	Medicago truncatula
13	G1038	7283684	5.20E-36	Glycine max
13	G1038	7218448	8.80E-36	Sorghum bicolor
13	G1038	572293	3.30E-35	Oryza sativa
13	G1038	8901641	4.30E-28	Hordeum vulgare
13	G1038	9962201	2.20E-16	Cryptomeria japonica
13	G1038	7614196	6.50E-11	Lotus japonicus
13	G1038	9291272	0.00015	Lycopersicon hirsutum
13	G1038	8122498	0.0005	Lycopersicon esculentum
13	G1038	9883662	0.68	Triticum aestivum
15	G438	7209474	8.70E-204	Oryza sativa
15	G438	7209911	2.20E-142	Physcomitrella patens
15	G438	7571387	2.30E-80	Medicago truncatula
15	G438	8330425	3.00E-66	Mesembryanthemum crystallinum
15	G438	6531152	1.60E-64	Lycopersicon esculentum
15	G438	6726825	4.70E-61	Glycine max
15	G438	5269007	7.00E-54	Zea mays
15	G438	9253000	1.70E-47	Solanum tuberosum
15	G438	8967371	4.40E-46	Hordeum vulgare
15	G438	2963336	1.60E-34	Pinus taeda
17	G571	6288681	1.50E-70	Nicotiana tabacum
17	G571	297019	1.60E-68	Zea mays
17	G571	10423526	2.20E-61	Oryza sativa
17	G571	5926681	4.20E-61	Triticum aestivum
17	G571	4959969	1.90E-59	Lycopersicon esculentum
17	G571	1372965	1.20E-56	Vicia faba
17	G571	8098832	1.20E-46	Hordeum vulgare
17	G571	9566058	2.00E-43	Glycine max
17	G571	765198	1.50E-41	Solanum tuberosum
17	G571	19679	3.80E-41	Nicotiana sp.
19	G748	853689	7.00E-87	Cucurbita maxima
19	G748	7242897	3.90E-59	Oryza sativa
19	G748	5888560	1.20E-45	Lycopersicon esculentum
19	G748	6341666	5.60E-38	Glycine max
19	G748	10700058	1.10E-36	Medicago truncatula
19	G748	7535776	5.00E-33	Sorghum bicolor
19	G748	9419494	2.10E-31	Hordeum vulgare
19	G748	9410157	1.00E-28	Triticum aestivum
19	G748	3929324	4.30E-25	Dendrobium grex Madame Thong-IN
19	G748	10449922	2.30E-23	Solanum tuberosum
21	G431	7340349	9.90E-177	Brassica oleracea
21	G431	3462611	1.20E-112	Pisum sativum
21	G431	310568	1.50E-112	Glycine max
21	G431	2251078	1.90E-107	Nicotiana tabacum
21	G431	4098239	1.20E-104	Lycopersicon esculentum
21	G431	1008878	4.90E-62	Zea mays
21	G431	6942299	7.90E-62	Triticum aestivum

Figure 3C

SEQ ID No.	GID	Genbank NID	P-value	Species
21	G431	3327239	1.90E-61	Oryza sativa
21	G431	3928842	1.60E-59	Picea abies
21	G431	2522483	2.30E-59	Hordeum vulgare
23	G187	9304207	2.10E-35	Sorghum bicolor
23	G187	9444636	3.20E-34	Triticum aestivum
23	G187	5058292	3.60E-34	Glycine max
23	G187	7721184	2.40E-32	Lotus japonicus
23	G187	7562279	1.20E-31	Medicago truncatula
23	G187	8105974	3.00E-29	Lycopersicon esculentum
23	G187	9049477	1.60E-27	Oryza sativa
23	G187	9187621	1.60E-23	Solanum tuberosum
23	G187	5268376	5.60E-23	Zea mays
23	G187	4894964	1.70E-22	Avena sativa
25	G470	6917173	4.80E-78	Lycopersicon pennellii
25	G470	8827792	8.50E-70	Glycine max
25	G470	5272309	7.40E-69	Lycopersicon esculentum
25	G470	7563870	6.70E-68	Medicago truncatula
25	G470	5296108	5.50E-65	Zea mays
25	G470	7339690	7.40E-57	Oryza sativa
25	G470	5047367	1.30E-51	Gossypium hirsutum
25	G470	9856054	9.70E-50	Sorghum bicolor
25	G470	3857884	1.10E-38	Populus balsamifera subsp. trichocarpa
25	G470	8174666	6.40E-37	Hordeum vulgare
27	G615	5566284	2.00E-28	Linaria vulgaris
27	G615	6358617	3.20E-27	Antirrhinum graniticum
27	G615	6358613	1.40E-26	Antirrhinum majus subsp. cirrhigerum
27	G615	6358545	8.60E-26	Digitalis purpurea
27	G615	6358538	1.40E-25	Antirrhinum braun-blauquetii
27	G615	6358541	1.40E-25	Misopates orontium
27	G615	6358542	1.40E-25	Antirrhinum molle
27	G615	6358573	1.40E-25	Misopates calycinum
27	G615	6358546	1.80E-25	Antirrhinum siculum
27	G615	2826867	2.70E-25	Antirrhinum majus
29	G1073	7238733	2.70E-55	Medicago truncatula
29	G1073	10843924	1.50E-44	Glycine max
29	G1073	7615218	2.00E-42	Lotus japonicus
29	G1073	7333102	3.40E-34	Lycopersicon esculentum
29	G1073	9689692	8.60E-28	Pinus taeda
29	G1073	9445090	4.30E-25	Triticum aestivum
29	G1073	9252370	2.80E-24	Solanum tuberosum
29	G1073	5042437	5.80E-21	Oryza sativa
29	G1073	7536402	6.70E-20	Sorghum bicolor
29	G1073	9662742	2.70E-19	Secale cereale
31	G1493	7614196	2.20E-50	Lotus japonicus
31	G1493	9986889	6.10E-48	Glycine max
31	G1493	8748344	2.20E-38	Medicago truncatula
31	G1493	572293	1.70E-37	Oryza sativa
31	G1493	7218448	5.70E-33	Sorghum bicolor
31	G1493	9291284	9.70E-32	Lycopersicon hirsutum
31	G1493	8380453	1.60E-30	Gossypium arboreum
31	G1493	8901641	1.70E-30	Hordeum vulgare
31	G1493	9962201	6.90E-17	Cryptomeria japonica
31	G1493	8122498	1.50E-08	Lycopersicon esculentum

Figure 3D

SEQ ID No.	GID	Genbank NID	P-value	Species
33	G993	7643366	1.20E-58	Medicago truncatula
33	G993	8329389	1.00E-49	Mesembryanthemum crystallinum
33	G993	8669779	6.10E-49	Glycine max
33	G993	9851335	6.30E-43	Sorghum bicolor
33	G993	4384549	5.20E-40	Lycopersicon esculentum
33	G993	10450225	3.70E-39	Solanum tuberosum
33	G993	8902194	2.50E-34	Hordeum vulgare
33	G993	7719409	1.30E-32	Lotus japonicus
33	G993	8749037	5.20E-32	Citrus x paradisi
33	G993	9247126	1.30E-30	Oryza sativa
35	G867	7643366	2.20E-57	Medicago truncatula
35	G867	8329389	1.10E-50	Mesembryanthemum crystallinum
35	G867	8669779	2.70E-46	Glycine max
35	G867	10450225	3.60E-41	Solanum tuberosum
35	G867	9851335	2.80E-40	Sorghum bicolor
35	G867	9430646	7.20E-40	Lycopersicon esculentum
35	G867	8902194	1.60E-34	Hordeum vulgare
35	G867	7722547	1.30E-33	Lotus japonicus
35	G867	7324245	3.90E-32	Lycopersicon pennellii
35	G867	8749037	1.40E-31	Citrus x paradisi
37	G1930	7643366	9.70E-57	Medicago truncatula
37	G1930	8329389	4.50E-47	Mesembryanthemum crystallinum
37	G1930	6069592	1.10E-46	Glycine max
37	G1930	10450225	6.50E-42	Solanum tuberosum
37	G1930	9430646	8.20E-39	Lycopersicon esculentum
37	G1930	9851335	1.80E-38	Sorghum bicolor
37	G1930	7722547	4.70E-34	Lotus japonicus
37	G1930	7324245	1.20E-32	Lycopersicon pennellii
37	G1930	8902194	3.00E-31	Hordeum vulgare
37	G1930	9697984	4.60E-29	Triticum aestivum
39	G1594	3327268	2.60E-74	Ipomoea nil
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39	G1594	4887609	1.50E-47	Oryza sativa
39	G1594	1814233	4.00E-46	Solanum tuberosum
39	G1594	4589883	6.30E-43	Nicotiana tabacum
39	G1594	4098241	6.70E-43	Lycopersicon esculentum
39	G1594	3928842	2.00E-42	Picea abies
39	G1594	4099825	2.60E-42	Picea mariana
39	G1594	4240538	1.70E-41	Zea mays
39	G1594	1946219	1.90E-41	Malus domestica
41	G391	7209474	4.70E-194	Oryza sativa
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41	G391	7560927	8.70E-67	Medicago truncatula
41	G391	10808354	1.50E-61	Solanum tuberosum
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41	G391	8330425	8.60E-59	Mesembryanthemum crystallinum
41	G391	8284059	8.70E-57	Glycine max
41	G391	5269007	8.10E-46	Zea mays
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41	G391	2963336	2.10E-37	Pinus taeda
43	G390	7209474	2.50E-166	Oryza sativa
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43	G390	7560927	5.80E-81	Medicago truncatula

Figure 3E

SEQ ID No.	GID	Genbank NID	P-value	Species
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43	G390	9466042	1.60E-59	Hordeum vulgare
43	G390	8284059	1.00E-57	Glycine max
43	G390	8330425	2.60E-44	Mesembryanthemum crystallinum
43	G390	5269007	4.60E-44	Zea mays
43	G390	2963336	4.90E-43	Pinus taeda
45	G1548	7209474	5.90E-169	Oryza sativa
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45	G1548	9253000	1.60E-76	Solanum tuberosum
45	G1548	9820423	1.40E-67	Glycine max
45	G1548	7570825	8.40E-67	Medicago truncatula
45	G1548	9456848	2.70E-55	Lycopersicon esculentum
45	G1548	9419425	1.40E-47	Hordeum vulgare
45	G1548	6626571	3.50E-46	Zea mays
45	G1548	8330425	4.20E-46	Mesembryanthemum crystallinum
45	G1548	3853847	2.70E-42	Populus tremula x Populus tremuloides

MBI0018 Sequence Listing.ST25
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Keddie, James
Ratcliffe, Oliver
Heard, Jacqueline
Samaha, Raymond
Yu, Guo-Liang
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gac	ggc	gat	tta	gct	ttt	ctt	gaa	gct	cac	tca	aag	gcc	gag	atc	gtc	497
Asp	Gly	Asp	Leu	Ala	Phe	Leu	Glu	Ala	His	Ser	Lys	Ala	Glu	Ile	Val	
	125					130						135				
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Asp	Met	Leu	Arg	Lys	His	Thr	Tyr	Ala	Asp	Glu	Leu	Glu	Gln	Asn	Asn	
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aaa	cgg	cag	ttg	ttt	ctc	tcc	gtc	gac	gct	aac	gga	aaa	cgt	aac	gga	593
Lys	Arg	Gln	Leu	Phe	Leu	Ser	Val	Asp	Ala	Asn	Gly	Lys	Arg	Asn	Gly	
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tcg	agt	act	act	caa	aac	gac	aaa	ggt	tta	aag	acg	tgt	gaa	ggt	ctt	641
Ser	Ser	Thr	Thr	Gln	Asn	Asp	Lys	Val	Leu	Lys	Thr	Cys	Glu	Val	Leu	
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ttc	gag	aag	gct	ggt	aca	cct	agc	gac	ggt	ggg	aag	cta	aac	cgt	ctc	689
Phe	Glu	Lys	Ala	Val	Thr	Pro	Ser	Asp	Val	Gly	Lys	Leu	Asn	Arg	Leu	
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Val	Ile	Pro	Lys	Gln	His	Ala	Glu	Lys	His	Phe	Pro	Leu	Pro	Ser	Pro	
	205					210					215					
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Ser	Pro	Ala	Val	Thr	Lys	Gly	Val	Leu	Ile	Asn	Phe	Glu	Asp	Val	Asn	
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Gly	Lys	Val	Trp	Arg	Phe	Arg	Tyr	Ser	Tyr	Trp	Asn	Ser	Ser	Gln	Ser	
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Tyr	Val	Leu	Thr	Lys	Gly	Trp	Ser	Arg	Phe	Val	Lys	Glu	Lys	Asn	Leu	
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cga	gcc	ggt	gat	ggt	ggt	act	ttc	gag	aga	tcg	acc	gga	cta	gag	cgg	929
Arg	Ala	Gly	Asp	Val	Val	Thr	Phe	Glu	Arg	Ser	Thr	Gly	Leu	Glu	Arg	
		270					275					280				
cag	tta	tat	att	gat	tgg	aaa	ggt	cgg	tct	ggt	ccg	aga	gaa	aac	ccg	977
Gln	Leu	Tyr	Ile	Asp	Trp	Lys	Val	Arg	Ser	Gly	Pro	Arg	Glu	Asn	Pro	
	285				290						295					
ggt	cag	gtg	gtg	ggt	cgg	ctt	ttc	gga	ggt	gat	atc	ttt	aat	gtg	acc	1025
Val	Gln	Val	Val	Val	Arg	Leu	Phe	Gly	Val	Asp	Ile	Phe	Asn	Val	Thr	
	300				305					310				315		
acc	gtg	aag	cca	aac	gac	gtc	gtg	gcc	ggt	tgc	ggt	gga	aag	aga	tct	1073
Thr	Val	Lys	Pro	Asn	Asp	Val	Val	Ala	Val	Cys	Gly	Gly	Lys	Arg	Ser	
				320					325					330		
cga	gat	ggt	gat	gat	atg	ttt	gcg	tta	cgg	tgt	tcc	aag	aag	cag	gcg	1121
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MBI0018 Sequence Listing.ST25

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 35 40 45

Pro Glu Asn Gly Leu Glu Thr Glu Ser Arg Lys Leu Pro Ser Ser Lys
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Tyr Lys Gly Val Val Pro Gln Pro Asn Gly Arg Trp Gly Ala Gln Ile
 65 70 75 80

Tyr Glu Lys His Gln Arg Val Trp Leu Gly Thr Phe Asn Glu Gln Glu
 85 90 95

Glu Ala Ala Arg Ser Tyr Asp Ile Ala Ala Cys Arg Phe Arg Gly Arg
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Asp Ala Val Val Asn Phe Lys Asn Val Leu Glu Asp Gly Asp Leu Ala
 115 120 125

Phe Leu Glu Ala His Ser Lys Ala Glu Ile Val Asp Met Leu Arg Lys
 130 135 140

His Thr Tyr Ala Asp Glu Leu Glu Gln Asn Asn Lys Arg Gln Leu Phe
 145 150 155 160

Leu Ser Val Asp Ala Asn Gly Lys Arg Asn Gly Ser Ser Thr Thr Gln
 165 170 175

Asn Asp Lys Val Leu Lys Thr Cys Glu Val Leu Phe Glu Lys Ala Val
 180 185 190

Thr Pro Ser Asp Val Gly Lys Leu Asn Arg Leu Val Ile Pro Lys Gln
 195 200 205

His Ala Glu Lys His Phe Pro Leu Pro Ser Pro Ser Pro Ala Val Thr
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Lys Gly Val Leu Ile Asn Phe Glu Asp Val Asn Gly Lys Val Trp Arg
 225 230 235 240

MBI0018 Sequence Listing.ST25

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 Val Thr Phe Glu Arg Ser Thr Gly Leu Glu Arg Gln Leu Tyr Ile Asp
 275 280 285
 Trp Lys Val Arg Ser Gly Pro Arg Glu Asn Pro Val Gln Val Val Val
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 Arg Leu Phe Gly Val Asp Ile Phe Asn Val Thr Thr Val Lys Pro Asn
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 ctg ttt gga tcc gac gaa ctc gct acc gct ttg tcc tcg gag ttg ctt 258
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 40 45 50
 ccg cgt att cga aaa gct gag gat aat ttc tct ctt agt gtc atc aaa 306
 Pro Arg Ile Arg Lys Ala Glu Asp Asn Phe Ser Leu Ser Val Ile Lys
 55 60 65 70
 tcc aaa atc gct tct cat cct ttg tat cct cgc tta ctc caa acc tac 354
 Ser Lys Ile Ala Ser His Pro Leu Tyr Pro Arg Leu Leu Gln Thr Tyr
 75 80 85
 atc gat tgc caa aag gtg gga gcg cct atg gaa ata gcg tgt ata ttg 402
 Ile Asp Cys Gln Lys Val Gly Ala Pro Met Glu Ile Ala Cys Ile Leu
 90 95 100
 gaa gag att cag cga gag aac cat gtg tac aag aga gat gtt gct cca 450
 Glu Glu Ile Gln Arg Glu Asn His Val Tyr Lys Arg Asp Val Ala Pro
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MBI0018 Sequence Listing.ST25

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 Tyr Cys Asp Ile Leu Val Lys Tyr Lys Thr Asp Leu Ala Arg Pro Phe
 135 140 145 150

gac gag gct aca act ttc ata aac aag att gaa atg cag ctt cag aac 594
 Asp Glu Ala Thr Thr Phe Ile Asn Lys Ile Glu Met Gln Leu Gln Asn
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ttg tgc act ggt cca gcg tct gct aca gct ctt tca gat gat ggt gcg 642
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gtt tca tct gac gag gaa ctg aga gaa gat gat gac ata gca gcg gat 690
 Val Ser Ser Asp Glu Glu Leu Arg Glu Asp Asp Asp Ile Ala Ala Asp
 185 190 195

gac agc caa caa aga agc aat gac cgc gat ctg aag gac cag cta cta 738
 Asp Ser Gln Gln Arg Ser Asn Asp Arg Asp Leu Lys Asp Gln Leu Leu
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cgc aaa ttt ggt agc cat atc agt tca ttg aaa ctc gag ttc tct aaa 786
 Arg Lys Phe Gly Ser His Ile Ser Ser Leu Lys Leu Glu Phe Ser Lys
 215 220 225 230

aag aag aag aaa ggg aag cta cca aga gaa gca aga caa gcg ttg ctc 834
 Lys Lys Lys Lys Gly Lys Leu Pro Arg Glu Ala Arg Gln Ala Leu Leu
 235 240 245

gat tgg tgg aat gtt cat aat aaa tgg cct tac cct act gaa ggc gac 882
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 250 255 260

aaa ata gct ctg gct gaa gaa aca ggt ttg gat caa aaa caa atc aac 930
 Lys Ile Ala Leu Ala Glu Glu Thr Gly Leu Asp Gln Lys Gln Ile Asn
 265 270 275

aat tgg ttt ata aac caa agg aaa cgc cat tgg aag cct tcg gag aac 978
 Asn Trp Phe Ile Asn Gln Arg Lys Arg His Trp Lys Pro Ser Glu Asn
 280 285 290

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 295 300 305 310

gaa tga aaagagagac atgggattgt gcattgtata atttttacac tgttttccca 1082
 Glu

agaaaagaaa acagtaaaaa gcttttggt aatgggacat catcggaat gaatggaacc 1142

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tattatgtca ctaatcttcc aatgggtccaa aatgatagat ttcttatttg tattgaacct 1262

tacttagata gctgatgtgt caactaaata atttattttc atccttatac tacttgtatc 1322

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MBI0018 Sequence Listing.ST25

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 50 55 60

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 65 70 75 80

Arg Leu Leu Gln Thr Tyr Ile Asp Cys Gln Lys Val Gly Ala Pro Met
 85 90 95

Glu Ile Ala Cys Ile Leu Glu Glu Ile Gln Arg Glu Asn His Val Tyr
 100 105 110

Lys Arg Asp Val Ala Pro Leu Ser Cys Phe Gly Ala Asp Pro Glu Leu
 115 120 125

Asp Glu Phe Met Glu Thr Tyr Cys Asp Ile Leu Val Lys Tyr Lys Thr
 130 135 140

Asp Leu Ala Arg Pro Phe Asp Glu Ala Thr Thr Phe Ile Asn Lys Ile
 145 150 155 160

Glu Met Gln Leu Gln Asn Leu Cys Thr Gly Pro Ala Ser Ala Thr Ala
 165 170 175

Leu Ser Asp Asp Gly Ala Val Ser Ser Asp Glu Glu Leu Arg Glu Asp
 180 185 190

Asp Asp Ile Ala Ala Asp Asp Ser Gln Gln Arg Ser Asn Asp Arg Asp
 195 200 205

Leu Lys Asp Gln Leu Leu Arg Lys Phe Gly Ser His Ile Ser Ser Leu
 210 215 220

Lys Leu Glu Phe Ser Lys Lys Lys Lys Gly Lys Leu Pro Arg Glu
 225 230 235 240

Ala Arg Gln Ala Leu Leu Asp Trp Trp Asn Val His Asn Lys Trp Pro
 245 250 255

Tyr Pro Thr Glu Gly Asp Lys Ile Ala Leu Ala Glu Glu Thr Gly Leu
 260 265 270

Asp Gln Lys Gln Ile Asn Asn Trp Phe Ile Asn Gln Arg Lys Arg His
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agc gag att aag aag aga gct aag aga aac act cta tcg tcc ctt cct 517
Ser Glu Ile Lys Lys Arg Ala Lys Arg Asn Thr Leu Ser Ser Leu Pro
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caa gaa acc caa cct ttg agg aaa gtc cgt att att gtg aat gat cct 565
Gln Glu Thr Gln Pro Leu Arg Lys Val Arg Ile Ile Val Asn Asp Pro
          35          40          45

tat gct act gat gat tcc tct agt gat gag gaa gag ctt aag gtt cct 613
Tyr Ala Thr Asp Asp Ser Ser Ser Asp Glu Glu Glu Leu Lys Val Pro
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Lys Pro Arg Lys Met Lys Arg Ile Val Arg Glu Ile Asn Phe Pro Ser
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atg gaa gtt tct gaa cag cct tct gag agt tct tct cag gac agt act 709
Met Glu Val Ser Glu Gln Pro Ser Ser Glu Ser Ser Gln Asp Ser Thr
          80          85          90

aaa act gat ggc aag ata gct gtg tca gct tct cct gct gtt cct agg 757
Lys Thr Asp Gly Lys Ile Ala Val Ser Ala Ser Pro Ala Val Pro Arg
95          100          105          110

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Lys Lys Pro Val Gly Val Arg Gln Arg Lys Trp Gly Lys Trp Ala Ala
          115          120          125

gag att aga gat cct att aag aaa act agg act tgg ttg ggt act ttt 853
Glu Ile Arg Asp Pro Ile Lys Lys Thr Arg Thr Trp Leu Gly Thr Phe
          130          135          140

gat act ctt gaa gaa gct gct aaa gct tat gat gct aag aag ctt gag 901
Asp Thr Leu Glu Glu Ala Ala Lys Ala Tyr Asp Ala Lys Lys Leu Glu
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ttt gat gct att gtt gct gga aat gtg tcc act act aaa cgt gat gtt 949
Phe Asp Ala Ile Val Ala Gly Asn Val Ser Thr Thr Lys Arg Asp Val
          160          165          170

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Ser Ser Ser Glu Thr Ser Gln Cys Ser Arg Ser Ser Pro Val Val Pro
175          180          185          190

gtt gag caa gat gac act tct gca tca gct ctc act tgt gtc aac aac 1045

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MBI0018 Sequence Listing.ST25

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cct gct ggt gga aac aag gaa acg ttg ttc gat ttc gac ttt act aat 1141
 Pro Ala Gly Gly Asn Lys Glu Thr Leu Phe Asp Phe Asp Phe Thr Asn
 225 230 235

cta cag atc cct gat ttt ggt ttc ttg gca gag gag caa caa gac cta 1189
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 255 260 265 270

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 275 280 285

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 Asp Phe Asp Phe Ala Asp Val Glu Asp Leu Gln Leu Ala Asp Ser Ser
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 Phe Gly Phe Leu Asp Gln Leu Ala Pro Ile Asn Ile Ser Cys Pro Leu
 305 310 315

aaa agt ttt gca gct tca tag gatcttgctt agtaaatgtta agtgagaaga 1432
 Lys Ser Phe Ala Ala Ser
 320

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 35 40 45

Thr Asp Asp Ser Ser Ser Asp Glu Glu Glu Leu Lys Val Pro Lys Pro
 50 55 60

Arg Lys Met Lys Arg Ile Val Arg Glu Ile Asn Phe Pro Ser Met Glu
 65 70 75 80

Val Ser Glu Gln Pro Ser Glu Ser Ser Ser Gln Asp Ser Thr Lys Thr
 85 90 95

Asp Gly Lys Ile Ala Val Ser Ala Ser Pro Ala Val Pro Arg Lys Lys
 100 105 110

MBI0018 Sequence Listing.ST25

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145 150 155 160

Ala Ile Val Ala Gly Asn Val Ser Thr Thr Lys Arg Asp Val Ser Ser
165 170 175

Ser Glu Thr Ser Gln Cys Ser Arg Ser Ser Pro Val Val Pro Val Glu
180 185 190

Gln Asp Asp Thr Ser Ala Ser Ala Leu Thr Cys Val Asn Asn Pro Asp
195 200 205

Asp Val Ser Thr Val Ala Pro Thr Ala Pro Thr Pro Asn Val Pro Ala
210 215 220

Gly Gly Asn Lys Glu Thr Leu Phe Asp Phe Asp Phe Thr Asn Leu Gln
225 230 235 240

Ile Pro Asp Phe Gly Phe Leu Ala Glu Glu Gln Gln Asp Leu Asp Phe
245 250 255

Asp Cys Phe Leu Ala Asp Asp Gln Phe Asp Asp Phe Gly Leu Leu Asp
260 265 270

Asp Ile Gln Gly Phe Glu Asp Asn Gly Pro Ser Ala Leu Pro Asp Phe
275 280 285

Asp Phe Ala Asp Val Glu Asp Leu Gln Leu Ala Asp Ser Ser Phe Gly
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Met Ala Met Gln Glu Arg Cys Glu Ser
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cct tac aaa aag aga gta aag gtg gaa gaa aac att gac aat gta aaa Pro Tyr Lys Lys Arg Val Lys Val Glu Glu Asn Ile Asp Asn Val Lys 270 275 280	930
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<400> 12

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35 40 45

Glu Ala Leu Lys Leu Tyr Gly Arg Ala Trp Arg Arg Ile Glu Glu His
50 55 60

Val Gly Thr Lys Thr Ala Val Gln Ile Arg Ser His Ala Gln Lys Phe
65 70 75 80

Phe Thr Lys Val Ala Arg Asp Phe Gly Val Ser Ser Glu Ser Ile Glu
85 90 95

Ile Pro Pro Pro Arg Pro Lys Arg Lys Pro Met His Pro Tyr Pro Arg
100 105 110

Lys Leu Val Ile Pro Asp Ala Lys Glu Met Val Tyr Ala Glu Leu Thr
115 120 125

Gly Ser Lys Leu Ile Gln Asp Glu Asp Asn Arg Ser Pro Thr Ser Val
130 135 140

Leu Ser Ala His Gly Ser Asp Gly Leu Gly Ser Ile Gly Ser Asn Ser
145 150 155 160

Pro Asn Ser Ser Ser Ala Glu Leu Ser Ser His Thr Glu Glu Ser Leu
165 170 175

Ser Leu Glu Ala Glu Thr Lys Gln Ser Leu Lys Leu Phe Gly Lys Thr
180 185 190

Phe Val Val Gly Asp Tyr Asn Ser Ser Met Ser Cys Asp Asp Ser Glu
195 200 205

Asp Gly Lys Lys Lys Leu Tyr Ser Glu Thr Gln Ser Leu Gln Cys Ser
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Ser Ser Thr Ser Glu Asn Ala Glu Thr Glu Val Val Val Ser Glu Phe
225 230 235 240

Lys Arg Ser Glu Arg Ser Ala Phe Ser Gln Leu Lys Ser Ser Val Thr

MBI0018 Sequence Listing.ST25

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Glu Met Asn Asn Met Arg Gly Phe Met Pro Tyr Lys Lys Arg Val Lys
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 atg gag aaa agc ggc ttc tct ccc gtc ggt cta agg gtt ctt gtc gta 287
 Met Glu Lys Ser Gly Phe Ser Pro Val Gly Leu Arg Val Leu Val Val
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 Asp Asp Asp Pro Thr Trp Leu Lys Ile Leu Glu Lys Met Leu Lys Lys
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 Cys Ser Tyr Glu Val Thr Thr Cys Gly Leu Ala Arg Glu Ala Leu Arg
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 Leu Leu Arg Glu Arg Lys Asp Gly Tyr Asp Ile Val Ile Ser Asp Val
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 aac atg cct gac atg gat ggt ttc aag ctt ctt gag cat gtt ggt ctt 479
 Asn Met Pro Asp Met Asp Gly Phe Lys Leu Leu Glu His Val Gly Leu
 65 70 75 80
 gaa tta gac ctc cct gta ata atg atg tcg gtg gac ggc gaa aca agc 527
 Glu Leu Asp Leu Pro Val Ile Met Met Ser Val Asp Gly Glu Thr Ser
 85 90 95
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 Arg Val Met Lys Gly Val His Thr Gly Ala Cys Asp Tyr Leu Leu Lys
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 Pro Ile Arg Met Lys Glu Leu Lys Ile Ile Trp Gln His Val Leu Arg
 115 120 125
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 Lys Lys Leu Gln Glu Val Arg Asp Ile Glu Gly Cys Gly Tyr Glu Gly
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 gga gcg gat tgg atc act cga tac gat gaa gca cat ttt ctt gga ggt 719
 Gly Ala Asp Trp Ile Thr Arg Tyr Asp Glu Ala His Phe Leu Gly Gly
 145 150 155 160
 ggt gaa gat gtt tct ttt ggg aaa aag aga aaa gac ttt gac ttt gag 767
 Gly Glu Asp Val Ser Phe Gly Lys Lys Arg Lys Asp Phe Asp Phe Glu
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MBI0018 Sequence Listing.ST25

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tatctgagct ccagccac cttaattggt atggaaatga gcggctgcct gaccctgacg	1764
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MBI0018 Sequence Listing.ST25

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Cys Ser Tyr Glu Val Thr Thr Cys Gly Leu Ala Arg Glu Ala Leu Arg
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Leu Leu Arg Glu Arg Lys Asp Gly Tyr Asp Ile Val Ile Ser Asp Val
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Asn Met Pro Asp Met Asp Gly Phe Lys Leu Leu Glu His Val Gly Leu
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Glu Leu Asp Leu Pro Val Ile Met Met Ser Val Asp Gly Glu Thr Ser
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Arg Val Met Lys Gly Val His Thr Gly Ala Cys Asp Tyr Leu Leu Lys
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Pro Ile Arg Met Lys Glu Leu Lys Ile Ile Trp Gln His Val Leu Arg
115          120          125

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130          135          140

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145          150          155          160

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Gly Glu Asp Val Ser Phe Gly Lys Lys Arg Lys Asp Phe Asp Phe Glu
165          170          175

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Lys Lys Leu Leu Gln Asp Glu Ser Asp Pro Ser Ser Ser Ser Ser Lys
180          185          190

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Lys Ala Arg Val Val Trp Ser Phe Glu Leu His His Lys Phe Val Asn
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Ala Val Asn Gln Ile Gly Cys Asp His Lys Ala Gly Pro Lys Lys Ile
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MBI0018 Sequence Listing.ST25

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Glu Leu Lys Cys Tyr Ser Gly Gly Val Lys Asn Ala Asp Ser Ser Pro
260 265 270

Lys Asp Val Glu Val Asn Ser Gly Tyr Gln Ser Pro Gly Arg Ser Ser
275 280 285

Tyr Val Phe Ser Gly Gly Asn Ser Leu Ile Gln Lys Ala Thr Glu Ile
290 295 300

Asp Pro Lys Pro Leu Ala Ser Ala Ser Leu Ser Asp Pro Asn Thr Asp
305 310 315 320

Val Ile Met Pro Pro Lys Thr Lys Lys Thr Arg Ile Gly Phe Asp Pro
325 330 335

Pro Ile Ser Ser Ser Ala Phe Asp Ser Leu Leu Pro Trp Asn Asp Val
340 345 350

Pro Glu Val Leu Glu Ser Lys Pro Val Leu Tyr Glu Asn Ser Phe Leu
355 360 365

Gln Gln Gln Pro Leu Pro Ser Gln Ser Ser Tyr Val Ala Ile Ser Ala
370 375 380

Pro Ser Leu Met Glu Glu Glu Met Lys Pro Pro Tyr Glu Thr Pro Ala
385 390 395 400

Gly Gly Ser Ser Val Asn Ala Asp Glu Phe Leu Met Pro Gln Asp Lys
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gccaaagaag aagaagaagc tagaagaaac agtaaagttt gagacttttt ttgagggtcg 180
agctaaa atg gag atg gcg gtg gct aac cac cgt gag aga agc agt gac 229
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MBI0018 Sequence Listing.ST25

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cgg aag ctc tct gcg atg aat aaa ctg ttg atg gag gag aat gat agg Arg Lys Leu Ser Ala Met Asn Lys Leu Leu Met Glu Glu Asn Asp Arg 95 100 105 110	517
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aca act cct cag cat tcg ctt aga gat gcg aat agt cct gct gga ttg Thr Thr Pro Gln His Ser Leu Arg Asp Ala Asn Ser Pro Ala Gly Leu 145 150 155	661
ctc tca atc gca gag gag act ttg gca gag ttc cta tcc aag gct aca Leu Ser Ile Ala Glu Glu Thr Trp Leu Ala Glu Phe Leu Ser Lys Ala Thr 160 165 170	709
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gtt ttc act atg ttc ccg gct ggt aat ggt ggc aca atc gag ctt gtt Val Phe Thr Met Phe Pro Ala Gly Asn Gly Gly Thr Ile Glu Leu Val 240 245 250	949
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MBI0018 Sequence Listing.ST25

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cta gga cat aca att gaa cac gaa gaa atg cta gaa gtt gtt aga ctg Leu Gly His Thr Ile Glu His Glu Glu Met Leu Glu Val Val Arg Leu 515 520 525			1765
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625 630 635

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Gln Phe Pro Phe Glu Asn Asn Leu Gln Glu Asn Val Ala Gly Met Ala
640 645 650

tgt cag tat gtg agg agc gtg atc tca tca gtt caa cgt gtt gca atg 2197
Cys Gln Tyr Val Arg Ser Val Ile Ser Ser Val Gln Arg Val Ala Met
655 660 665

gcg atc tca ccg tct ggg ata agc ccg agt ctg ggc tcc aaa ttg tcc 2245
Ala Ile Ser Pro Ser Gly Ile Ser Pro Ser Leu Gly Ser Lys Leu Ser
675 680 685

cca gga tct cct gaa gct gtt act ctt gct cag tgg atc tct caa agt 2293
Pro Gly Ser Pro Glu Ala Val Thr Leu Ala Gln Trp Ile Ser Gln Ser
690 695 700

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Tyr Ser His His Leu Gly Ser Glu Leu Leu Thr Ile Asp Ser Leu Gly
705 710 715

agc gac gac tcg gta cta aaa ctt cta tgg gat cac caa gat gcc atc 2389
Ser Asp Asp Ser Val Leu Lys Leu Leu Trp Asp His Gln Asp Ala Ile
720 725 730

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Leu Cys Cys Ser Leu Lys Pro Gln Pro Val Phe Met Phe Ala Asn Gln
735 740 745 750

gct ggt cta gac atg cta gag aca aca ctt gta gcc tta caa gat ata 2485
Ala Gly Leu Asp Met Leu Glu Thr Thr Leu Val Ala Leu Gln Asp Ile
755 760 765

aca ctc gaa aag ata ttc gat gaa tcg ggt cgt aag gct atc tgt tcg 2533
Thr Leu Glu Lys Ile Phe Asp Glu Ser Gly Arg Lys Ala Ile Cys Ser
770 775 780

gac ttc gcc aag cta atg caa cag gga ttt gct tgc ttg cct tca gga 2581
Asp Phe Ala Lys Leu Met Gln Gln Gly Phe Ala Cys Leu Pro Ser Gly
785 790 795

atc tgt gtg tca acg atg gga aga cat gtg agt tat gaa caa gct gtt 2629
Ile Cys Val Ser Thr Met Gly Arg His Val Ser Tyr Glu Gln Ala Val
800 805 810

gct tgg aaa gtg ttt gct gca tct gaa gaa aac aac aac aat ctg cat 2677
Ala Trp Lys Val Phe Ala Ala Ser Glu Glu Asn Asn Asn Asn Leu His
815 820 825 830

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Cys Leu Ala Phe Ser Phe Val Asn Trp Ser Phe Val
835 840

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MBI0018 Sequence Listing.ST25

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Gln Val Glu Ala Leu Glu Arg Val Tyr Ala Glu Cys Pro Lys Pro Ser
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Ser Leu Arg Arg Gln Gln Leu Ile Arg Glu Cys Ser Ile Leu Ala Asn
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Ile Glu Pro Lys Gln Ile Lys Val Trp Phe Gln Asn Arg Arg Cys Arg
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Asp Lys Gln Arg Lys Glu Ala Ser Arg Leu Gln Ser Val Asn Arg Lys
 85 90 95

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 100 105 110

Lys Gln Val Ser Gln Leu Val Cys Glu Asn Gly Tyr Met Lys Gln Gln
 115 120 125

Leu Thr Thr Val Val Asn Asp Pro Ser Cys Glu Ser Val Val Thr Thr
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Pro Gln His Ser Leu Arg Asp Ala Asn Ser Pro Ala Gly Leu Leu Ser
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Ala Val Asp Trp Val Gln Met Pro Gly Met Lys Pro Gly Pro Asp Ser
 180 185 190

Val Gly Ile Phe Ala Ile Ser Gln Arg Cys Asn Gly Val Ala Ala Arg
 195 200 205

Ala Cys Gly Leu Val Ser Leu Glu Pro Met Lys Ile Ala Glu Ile Leu
 210 215 220

Lys Asp Arg Pro Ser Trp Phe Arg Asp Cys Arg Ser Leu Glu Val Phe
 225 230 235 240

Thr Met Phe Pro Ala Gly Asn Gly Gly Thr Ile Glu Leu Val Tyr Met
 245 250 255

Gln Thr Tyr Ala Pro Thr Thr Leu Ala Pro Ala Arg Asp Phe Trp Thr
 260 265 270

Leu Arg Tyr Thr Thr Ser Leu Asp Asn Gly Ser Phe Val Val Cys Glu
 275 280 285

Arg Ser Leu Ser Gly Ser Gly Ala Gly Pro Asn Ala Ala Ser Ala Ser
 290 295 300

Gln Phe Val Arg Ala Glu Met Leu Ser Ser Gly Tyr Leu Ile Arg Pro
 305 310 315 320

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Glu	Ala	Trp	Ser	Val	Pro	Asp	Val	Leu	Arg	Pro	Leu	Tyr	Glu	Ser	Ser	
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Lys	Val	Val	Ala	Gln	Lys	Met	Thr	Ile	Ser	Ala	Leu	Arg	Tyr	Ile	Arg	
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Gln	Leu	Ala	Gln	Glu	Ser	Asn	Gly	Glu	Val	Val	Tyr	Gly	Leu	Gly	Arg	
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His	Ser	Leu	Ala	Gln	Glu	Asp	Ala	Phe	Met	Ser	Arg	Asp	Val	His	Leu	
	530					535					540					
Leu	Gln	Ile	Cys	Thr	Gly	Ile	Asp	Glu	Asn	Ala	Val	Gly	Ala	Cys	Ser	
	545				550					555					560	
Glu	Leu	Ile	Phe	Ala	Pro	Ile	Asn	Glu	Met	Phe	Pro	Asp	Asp	Ala	Pro	
				565					570					575		
Leu	Val	Pro	Ser	Gly	Phe	Arg	Val	Ile	Pro	Val	Asp	Ala	Lys	Thr	Gly	
			580					585					590			
Asp	Val	Gln	Asp	Leu	Leu	Thr	Ala	Asn	His	Arg	Thr	Leu	Asp	Leu	Thr	
		595					600					605				
Ser	Ser	Leu	Glu	Val	Gly	Pro	Ser	Pro	Glu	Asn	Ala	Ser	Gly	Asn	Ser	
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Phe Ser Ser Ser Ser Ser Arg Cys Ile Leu Thr Ile Ala Phe Gln Phe
625 630 635 640

Pro Phe Glu Asn Asn Leu Gln Glu Asn Val Ala Gly Met Ala Cys Gln
645 650 655

Tyr Val Arg Ser Val Ile Ser Ser Val Gln Arg Val Ala Met Ala Ile
660 665 670

Ser Pro Ser Gly Ile Ser Pro Ser Leu Gly Ser Lys Leu Ser Pro Gly
675 680 685

Ser Pro Glu Ala Val Thr Leu Ala Gln Trp Ile Ser Gln Ser Tyr Ser
690 695 700

His His Leu Gly Ser Glu Leu Leu Thr Ile Asp Ser Leu Gly Ser Asp
705 710 715 720

Asp Ser Val Leu Lys Leu Leu Trp Asp His Gln Asp Ala Ile Leu Cys
725 730 735

Cys Ser Leu Lys Pro Gln Pro Val Phe Met Phe Ala Asn Gln Ala Gly
740 745 750

Leu Asp Met Leu Glu Thr Thr Leu Val Ala Leu Gln Asp Ile Thr Leu
755 760 765

Glu Lys Ile Phe Asp Glu Ser Gly Arg Lys Ala Ile Cys Ser Asp Phe
770 775 780

Ala Lys Leu Met Gln Gln Gly Phe Ala Cys Leu Pro Ser Gly Ile Cys
785 790 795 800

Val Ser Thr Met Gly Arg His Val Ser Tyr Glu Gln Ala Val Ala Trp
805 810 815

Lys Val Phe Ala Ala Ser Glu Glu Asn Asn Asn Asn Leu His Cys Leu
820 825 830

Ala Phe Ser Phe Val Asn Trp Ser Phe Val
835 840

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<213> Arabidopsis thaliana

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<223> G571

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cataatctct atctctttcc aagaatatag agaaaggaaa ataatatata agaattaaaa 120
gaaggtatat catcatctct ctagctagt atcaaagcac cgatcatcat atcatatatc 180

MBI0018 Sequence Listing.ST25

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tcttcatcat cttctgctgt tactatcata tcacacgctc tctcaaacat catcctatat      300
atagacttct cttcatcatc atcaa atg caa ggt cat cac cag aat cat cat      352
                               Met Gln Gly His His Gln Asn His His
                               1                               5

caa cac tta tca tca tcc tcc gcc acg tct tcc cat gga aac ttc atg      400
Gln His Leu Ser Ser Ser Ala Thr Ser Ser His Gly Asn Phe Met
10                               15                               20                               25

aac aaa gat ggg tat gat att gga gag ata gac cca tca ctc ttc ctc      448
Asn Lys Asp Gly Tyr Asp Ile Gly Glu Ile Asp Pro Ser Leu Phe Leu
                               30                               35                               40

tat ctt gat gga caa gga cat cat gat cct cca tca act gct cct tct      496
Tyr Leu Asp Gly Gln Gly His His Asp Pro Pro Ser Thr Ala Pro Ser
                               45                               50                               55

cct tta cat cat cat cac aca act cag aat ttg gcg atg aga cct cca      544
Pro Leu His His His His Thr Thr Gln Asn Leu Ala Met Arg Pro Pro
                               60                               65                               70

aca tcg acg ctc aac atc ttt cca tct cag cct atg cac ata gag cca      592
Thr Ser Thr Leu Asn Ile Phe Pro Ser Gln Pro Met His Ile Glu Pro
75                               80                               85

cct cct tct tct aca cac aat acc gat aat aca aga tta gtt ccg gct      640
Pro Pro Ser Ser Thr His Asn Thr Asp Asn Thr Arg Leu Val Pro Ala
90                               95                               100                               105

gct caa cct agt ggt tcc act cga cca gct tct gac ccg tcc atg gac      688
Ala Gln Pro Ser Gly Ser Thr Arg Pro Ala Ser Asp Pro Ser Met Asp
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ttg acc aat cat tct cag ttt cat caa cct cct caa ggt tct aaa tcc      736
Leu Thr Asn His Ser Gln Phe His Gln Pro Pro Gln Gly Ser Lys Ser
125                               130                               135

atc aag aag gaa ggg aac cgc aag ggt ctt gcc tca tcg gac cat gac      784
Ile Lys Lys Glu Gly Asn Arg Lys Gly Leu Ala Ser Ser Asp His Asp
140                               145                               150

ata cct aaa tcg tca gac cct aaa aca ttg aga aga cta gca caa aac      832
Ile Pro Lys Ser Ser Asp Pro Lys Thr Leu Arg Arg Leu Ala Gln Asn
155                               160                               165

aga gaa gca gca aga aaa agc aga tta cgt aaa aag gct tat gtt cag      880
Arg Glu Ala Ala Arg Lys Ser Arg Leu Arg Lys Lys Ala Tyr Val Gln
170                               175                               180                               185

caa ctc gag tca tgt agg atc aaa ctg acc caa cta gaa caa gag att      928
Gln Leu Glu Ser Cys Arg Ile Lys Leu Thr Gln Leu Glu Gln Glu Ile
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caa cgg gcc aga tcc caa ggc gta ttc ttt gga ggg tct ctt ata gga      976
Gln Arg Ala Arg Ser Gln Gly Val Phe Phe Gly Gly Ser Leu Ile Gly
205                               210                               215

gga gat caa cag caa ggt gga cta ccc att ggc cct ggc aac atc agc      1024
Gly Asp Gln Gln Gln Gly Gly Leu Pro Ile Gly Pro Gly Asn Ile Ser
220                               225                               230

tct gaa gca gcg gtg ttc gat atg gaa tat gcg agg tgg ctg gag gag      1072
Ser Glu Ala Ala Val Phe Asp Met Glu Tyr Ala Arg Trp Leu Glu Glu
235                               240                               245

cag cag agg cta tta aac gaa cta agg gtg gca aca caa gaa cac ttg      1120
Gln Gln Arg Leu Leu Asn Glu Leu Arg Val Ala Thr Gln Glu His Leu
250                               255                               260                               265

tcc gag aac gag ctt agg atg ttt gtg gac aca tgt tta gct cat tat      1168
Ser Glu Asn Glu Leu Arg Met Phe Val Asp Thr Cys Leu Ala His Tyr

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cac ctc att tct gga gca tgg aaa act cca gct gaa cgt tgc ttc ttg His Leu Ile Ser Gly Ala Trp Lys Thr Pro Ala Glu Arg Cys Phe Leu 300 305 310			1264
tgg atg ggt ggt ttc cgt cca tgc gag atc att aag gtg att gtg aac Trp Met Gly Gly Phe Arg Pro Ser Glu Ile Ile Lys Val Ile Val Asn 315 320 325			1312
cag ata gaa cca ttg acg gag caa cag ata gtt ggg ata tgt ggg ctg Gln Ile Glu Pro Leu Thr Glu Gln Gln Ile Val Gly Ile Cys Gly Leu 330 335 340 345			1360
caa cag tcc aca caa gag gcc gag gag gct ctc tgc caa ggc ctc gag Gln Gln Ser Thr Gln Glu Ala Glu Glu Ala Leu Ser Gln Gly Leu Glu 350 355 360			1408
gcg ttg aat caa tca ctt tcc gat agc att gtc tct gac tcc ctc ccg Ala Leu Asn Gln Ser Leu Ser Asp Ser Ile Val Ser Asp Ser Leu Pro 365 370 375			1456
cct gcc tcc gca cca ctt cct cct cat cta tcc aat ttc atg tca cac Pro Ala Ser Ala Pro Leu Pro Pro His Leu Ser Asn Phe Met Ser His 380 385 390			1504
atg tcc tta gct ctc aac aag ctc tct gct ctc gag ggc ttc gtt ctc Met Ser Leu Ala Leu Asn Lys Leu Ser Ala Leu Glu Gly Phe Val Leu 395 400 405			1552
cag gcg gat aat ttg agg cac caa acg atc cat agg ctg aac caa ttg Gln Ala Asp Asn Leu Arg His Gln Thr Ile His Arg Leu Asn Gln Leu 410 415 420 425			1600
ttg acg acc cgt caa gaa gca cgg tgt ctt cta gcc gtt gcg gag tac Leu Thr Thr Arg Gln Glu Ala Arg Cys Leu Leu Ala Val Ala Glu Tyr 430 435 440			1648
ttc cac cgt ctt caa gct cta agt tct ctc tgg cta gcc cgt cct cgg Phe His Arg Leu Gln Ala Leu Ser Ser Leu Trp Leu Ala Arg Pro Arg 445 450 455			1696
caa gat gga taa tactaaaaca actgatgaag gaaacaaaa acaaaaacaa Gln Asp Gly 460			1748
gagaataggt tgattagtta gccgccagct tgacctcttt atcatatata tcgtctctct			1808
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 <213> Arabidopsis thaliana

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Gly Glu Ile Asp Pro Ser Leu Phe Leu Tyr Leu Asp Gly Gln Gly His
35 40 45

MBI0018 Sequence Listing.ST25

His Asp Pro Pro Ser Thr Ala Pro Ser Pro Leu His His His His Thr
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 Thr Gln Asn Leu Ala Met Arg Pro Pro Thr Ser Thr Leu Asn Ile Phe
 65 70 75 80
 Pro Ser Gln Pro Met His Ile Glu Pro Pro Pro Ser Ser Thr His Asn
 85 90 95
 Thr Asp Asn Thr Arg Leu Val Pro Ala Ala Gln Pro Ser Gly Ser Thr
 100 105 110
 Arg Pro Ala Ser Asp Pro Ser Met Asp Leu Thr Asn His Ser Gln Phe
 115 120 125
 His Gln Pro Pro Gln Gly Ser Lys Ser Ile Lys Lys Glu Gly Asn Arg
 130 135 140
 Lys Gly Leu Ala Ser Ser Asp His Asp Ile Pro Lys Ser Ser Asp Pro
 145 150 155 160
 Lys Thr Leu Arg Arg Leu Ala Gln Asn Arg Glu Ala Ala Arg Lys Ser
 165 170 175
 Arg Leu Arg Lys Lys Ala Tyr Val Gln Gln Leu Glu Ser Cys Arg Ile
 180 185 190
 Lys Leu Thr Gln Leu Glu Gln Glu Ile Gln Arg Ala Arg Ser Gln Gly
 195 200 205
 Val Phe Phe Gly Gly Ser Leu Ile Gly Gly Asp Gln Gln Gln Gly Gly
 210 215 220
 Leu Pro Ile Gly Pro Gly Asn Ile Ser Ser Glu Ala Ala Val Phe Asp
 225 230 235 240
 Met Glu Tyr Ala Arg Trp Leu Glu Glu Gln Gln Arg Leu Leu Asn Glu
 245 250 255
 Leu Arg Val Ala Thr Gln Glu His Leu Ser Glu Asn Glu Leu Arg Met
 260 265 270
 Phe Val Asp Thr Cys Leu Ala His Tyr Asp His Leu Ile Asn Leu Lys
 275 280 285
 Ala Met Val Ala Lys Thr Asp Val Phe His Leu Ile Ser Gly Ala Trp
 290 295 300
 Lys Thr Pro Ala Glu Arg Cys Phe Leu Trp Met Gly Gly Phe Arg Pro
 305 310 315 320
 Ser Glu Ile Ile Lys Val Ile Val Asn Gln Ile Glu Pro Leu Thr Glu
 325 330 335
 Gln Gln Ile Val Gly Ile Cys Gly Leu Gln Gln Ser Thr Gln Glu Ala
 340 345 350

MBI0018 Sequence Listing.ST25

Glu Glu Ala Leu Ser Gln Gly Leu Glu Ala Leu Asn Gln Ser Leu Ser
355 360 365

Asp Ser Ile Val Ser Asp Ser Leu Pro Pro Ala Ser Ala Pro Leu Pro
370 375 380

Pro His Leu Ser Asn Phe Met Ser His Met Ser Leu Ala Leu Asn Lys
385 390 395 400

Leu Ser Ala Leu Glu Gly Phe Val Leu Gln Ala Asp Asn Leu Arg His
405 410 415

Gln Thr Ile His Arg Leu Asn Gln Leu Leu Thr Thr Arg Gln Glu Ala
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<223> G748

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Met Met Met Glu Thr Arg
1 5
gat cca gct att aag ctt ttc ggt atg aaa atc cct ttt ccg tcg gtt 163
Asp Pro Ala Ile Lys Leu Phe Gly Met Lys Ile Pro Phe Pro Ser Val
10 15 20
ttt gaa tcg gca gtt acg gtg gag gat gac gaa gaa gat gac tgg agc 211
Phe Glu Ser Ala Val Thr Val Glu Asp Asp Glu Glu Asp Asp Trp Ser
25 30 35
ggc gga gat gac aaa tca cca gag aag gta act cca gag tta tca gat 259
Gly Gly Asp Asp Lys Ser Pro Glu Lys Val Thr Pro Glu Leu Ser Asp
40 45 50
aag aac aac aac aac tgt aac gac aac agt ttt aac aat tcg aaa ccc 307
Lys Asn Asn Asn Asn Cys Asn Asp Asn Ser Phe Asn Asn Ser Lys Pro
55 60 65 70
gaa acc ttg gac aaa gag gaa gcg aca tca act gat cag ata gag agt 355
Glu Thr Leu Asp Lys Glu Glu Ala Thr Ser Thr Asp Gln Ile Glu Ser
75 80 85
agt gac acg cct gag gat aat cag cag acg aca cct gat ggt aaa acc 403
Ser Asp Thr Pro Glu Asp Asn Gln Gln Thr Thr Pro Asp Gly Lys Thr
90 95 100
cta aag aaa ccg act aag att cta ccg tgt ccg aga tgc aaa agc atg 451
Leu Lys Lys Pro Thr Lys Ile Leu Pro Cys Pro Arg Cys Lys Ser Met
105 110 115

MBI0018 Sequence Listing.ST25

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agg aat gtt cct gtg ggg gca gga cgt cgt aag aac aaa agc tca tct Arg Asn Val Pro Val Gly Ala Gly Arg Arg Lys Asn Lys Ser Ser Ser 155 160 165	595
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ctt gac ccg ggc tta cag gca aac aca agg gtc ttg agt ttt ggt ctc Leu Asp Pro Gly Leu Gln Ala Asn Thr Arg Val Leu Ser Phe Gly Leu 185 190 195	691
gaa gct cag cag cag cac gtt gct gct ccc atg aca cct gtt atg aag Glu Ala Gln Gln Gln His Val Ala Ala Pro Met Thr Pro Val Met Lys 200 205 210	739
cta caa gaa gat caa aag gtc tca aac ggt gct agg aac agg ttt cac Leu Gln Glu Asp Gln Lys Val Ser Asn Gly Ala Arg Asn Arg Phe His 215 220 225 230	787
ggg tta gcg gat caa ccg ctt gta gct ccg gta gag aat gga gat gat Gly Leu Ala Asp Gln Arg Leu Val Ala Arg Val Glu Asn Gly Asp Asp 235 240 245	835
tgc tca agc gga tcc tct gtg acc acc tct aac aat cac tca gtg gat Cys Ser Ser Gly Ser Ser Val Thr Thr Ser Asn Asn His Ser Val Asp 250 255 260	883
gaa tca aga gca caa agc ggc agt gtt gtt gaa gca caa atg aac aac Glu Ser Arg Ala Gln Ser Gly Ser Val Val Glu Ala Gln Met Asn Asn 265 270 275	931
aac aac aac aat aac atg aat ggt tat gct tgc atc cca ggt gtt cca Asn Asn Asn Asn Asn Met Asn Gly Tyr Ala Cys Ile Pro Gly Val Pro 280 285 290	979
tgg cct tac acg tgg aat cca gcg atg cct cca cca ggt ttt tac ccg Trp Pro Tyr Thr Trp Asn Pro Ala Met Pro Pro Pro Gly Phe Tyr Pro 295 300 305 310	1027
cct cca ggg tat cca atg ccg ttt tac cct tac tgg acc atc cca atg Pro Pro Gly Tyr Pro Met Pro Phe Tyr Pro Tyr Trp Thr Ile Pro Met 315 320 325	1075
cta cca ccg cat caa tcc tca tcg cct ata agc caa aag tgt tca aat Leu Pro Pro His Gln Ser Ser Ser Pro Ile Ser Gln Lys Cys Ser Asn 330 335 340	1123
aca aac tct ccg act ctc gga aag cat ccg aga gat gaa gga tca tcg Thr Asn Ser Pro Thr Leu Gly Lys His Pro Arg Asp Glu Gly Ser Ser 345 350 355	1171
aaa aag gac aat gag aca gag cga aaa cag aag gcc ggg tgc gtt ctg Lys Lys Asp Asn Glu Thr Glu Arg Lys Gln Lys Ala Gly Cys Val Leu 360 365 370	1219
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tcg ata tgg aca aca ttg gga atc aag aac gag gcg atg tgc aaa gcc Ser Ile Trp Thr Thr Leu Gly Ile Lys Asn Glu Ala Met Cys Lys Ala 395 400 405	1315
ggg ggt atg ttc aaa ggg ttt gat cat aag aca aag atg tat aac aac Gly Gly Met Phe Lys Gly Phe Asp His Lys Thr Lys Met Tyr Asn Asn 410 415 420 425 430 435 440	1363

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410 415 420

gac aaa gct gag aac tcc cct gtt ctt tct gct aac cct gct gct cta 1411
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tca aga tca cac aat ttc cat gaa cag att tag agttacatat gtatatgtat 1464
 Ser Arg Ser His Asn Phe His Glu Gln Ile
 440 445

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 aactcttttc ttctttcttag tgattgcctt tattccttta catgttttgg ttctctgtac 1584
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Glu Glu Asp Asp Trp Ser Gly Gly Asp Asp Lys Ser Pro Glu Lys Val
 35 40 45

Thr Pro Glu Leu Ser Asp Lys Asn Asn Asn Asn Cys Asn Asp Asn Ser
 50 55 60

Phe Asn Asn Ser Lys Pro Glu Thr Leu Asp Lys Glu Glu Ala Thr Ser
 65 70 75 80

Thr Asp Gln Ile Glu Ser Ser Asp Thr Pro Glu Asp Asn Gln Gln Thr
 85 90 95

Thr Pro Asp Gly Lys Thr Leu Lys Lys Pro Thr Lys Ile Leu Pro Cys
 100 105 110

Pro Arg Cys Lys Ser Met Glu Thr Lys Phe Cys Tyr Tyr Asn Asn Tyr
 115 120 125

Asn Ile Asn Gln Pro Arg His Phe Cys Lys Ala Cys Gln Arg Tyr Trp
 130 135 140

Thr Ala Gly Gly Thr Met Arg Asn Val Pro Val Gly Ala Gly Arg Arg
 145 150 155 160

Lys Asn Lys Ser Ser Ser Ser His Tyr Arg His Ile Thr Ile Ser Glu
 165 170 175

Ala Leu Glu Ala Ala Arg Leu Asp Pro Gly Leu Gln Ala Asn Thr Arg
 180 185 190

MBI0018 Sequence Listing.ST25

Val Leu Ser Phe Gly Leu Glu Ala Gln Gln Gln His Val Ala Ala Pro
195 200 205

Met Thr Pro Val Met Lys Leu Gln Glu Asp Gln Lys Val Ser Asn Gly
210 215 220

Ala Arg Asn Arg Phe His Gly Leu Ala Asp Gln Arg Leu Val Ala Arg
225 230 235 240

Val Glu Asn Gly Asp Asp Cys Ser Ser Gly Ser Ser Val Thr Thr Ser
245 250 255

Asn Asn His Ser Val Asp Glu Ser Arg Ala Gln Ser Gly Ser Val Val
260 265 270

Glu Ala Gln Met Asn Asn Asn Asn Asn Asn Asn Met Asn Gly Tyr Ala
275 280 285

Cys Ile Pro Gly Val Pro Trp Pro Tyr Thr Trp Asn Pro Ala Met Pro
290 295 300

Pro Pro Gly Phe Tyr Pro Pro Pro Gly Tyr Pro Met Pro Phe Tyr Pro
305 310 315 320

Tyr Trp Thr Ile Pro Met Leu Pro Pro His Gln Ser Ser Ser Pro Ile
325 330 335

Ser Gln Lys Cys Ser Asn Thr Asn Ser Pro Thr Leu Gly Lys His Pro
340 345 350

Arg Asp Glu Gly Ser Ser Lys Lys Asp Asn Glu Thr Glu Arg Lys Gln
355 360 365

Lys Ala Gly Cys Val Leu Val Pro Lys Thr Leu Arg Ile Asp Asp Pro
370 375 380

Asn Glu Ala Ala Lys Ser Ser Ile Trp Thr Thr Leu Gly Ile Lys Asn
385 390 395 400

Glu Ala Met Cys Lys Ala Gly Gly Met Phe Lys Gly Phe Asp His Lys
405 410 415

Thr Lys Met Tyr Asn Asn Asp Lys Ala Glu Asn Ser Pro Val Leu Ser
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<223> G431

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Asp Asn Ser Asp Gly Pro Met Cys Pro Met Met Met Met Met Pro Pro
20      25      30

atc atg aca tca cat caa cat cat ggt cat gat cat caa cat caa caa      144
Ile Met Thr Ser His Gln His His Gly His Asp His Gln His Gln Gln
35      40      45

caa gaa cat gat ggt tat gca tat cag tca cac cac caa caa agt agt      192
Gln Glu His Asp Gly Tyr Ala Tyr Gln Ser His His Gln Gln Ser Ser
50      55      60

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Ser Leu Phe Leu Gln Ser Leu Ala Pro Pro Gln Gly Thr Lys Asn Lys
65      70      75      80

gtt gct tct tct tct tct cct tcc tct tgt gct cct gcc tat tct cta      288
Val Ala Ser Ser Ser Ser Pro Ser Ser Cys Ala Pro Ala Tyr Ser Leu
85      90      95

atg gag atc cat cat aac gaa atc gtt gca gga gga atc aac cct tgc      336
Met Glu Ile His His Asn Glu Ile Val Ala Gly Gly Ile Asn Pro Cys
100     105     110

tcc tct ttc tct tct tca gcc tct gtc aag gcc aag atc atg gct cat      384
Ser Ser Phe Ser Ser Ser Ala Ser Val Lys Ala Lys Ile Met Ala His
115     120     125

cct cac tac cac cgc ctc ttg gcc gct tat gtc aat tgt cag aag gtt      432
Pro His Tyr His Arg Leu Leu Ala Ala Tyr Val Asn Cys Gln Lys Val
130     135     140

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145     150     155     160

gcc gca gcc gca gcc gca tct atg ggg cca aca ggg tgt ctt ggt gaa      528
Ala Ala Ala Ala Ala Ala Ser Met Gly Pro Thr Gly Cys Leu Gly Glu
165     170     175

gat cca ggg ctt gat caa ttc atg gaa gct tac tgt gaa atg ctc gtt      576
Asp Pro Gly Leu Asp Gln Phe Met Glu Ala Tyr Cys Glu Met Leu Val
180     185     190

aag tat gag caa gag ctc tcc aaa cct ttc aag gaa gct atg gtc ttc      624
Lys Tyr Glu Gln Glu Leu Ser Lys Pro Phe Lys Glu Ala Met Val Phe
195     200     205

ctt caa cgt gtc gag tgt caa ttc aaa tcc ctc tct cta tcc tca cct      672
Leu Gln Arg Val Glu Cys Gln Phe Lys Ser Leu Ser Leu Ser Ser Pro
210     215     220

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Ser Ser Phe Ser Gly Tyr Gly Glu Thr Ala Ile Asp Arg Asn Asn Asn
225     230     235     240

ggg tca tcc gag gaa gaa gtc gat atg aac aat gaa ttt gta gat cca      768
Gly Ser Ser Glu Glu Glu Val Asp Met Asn Asn Glu Phe Val Asp Pro
245     250     255

caa gct gag gat aga gag ctt aaa gga cag ctc ttg cgc aag tac agt      816
Gln Ala Glu Asp Arg Glu Leu Lys Gly Gln Leu Leu Arg Lys Tyr Ser
260     265     270

ggt tac tta ggg agc ctc aag caa gag ttc atg aag aag agg aag aaa      864
Gly Tyr Leu Gly Ser Leu Lys Gln Glu Phe Met Lys Lys Arg Lys Lys
275     280     285

gga aag ctc cct aaa gaa gct cgt caa caa ctg ctt gat tgg tgg agc      912

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MBI0018 Sequence Listing.ST25

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 290 295 300

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 Arg His Tyr Lys Trp Pro Tyr Pro Ser Glu Gln Gln Lys Leu Ala Leu
 305 310 315 320

gcg gaa tca acg ggg ctg gac cag aaa cag ata aac aat tgg ttc ata 1008
 Ala Glu Ser Thr Gly Leu Asp Gln Lys Gln Ile Asn Asn Trp Phe Ile
 325 330 335

aac cag agg aaa cgg cat tgg aag ccg tcg gag gac atg cag ttt gta 1056
 Asn Gln Arg Lys Arg His Trp Lys Pro Ser Glu Asp Met Gln Phe Val
 340 345 350

gta atg gac gca aca cat cct cac cat tac ttc atg gat aat gtc ttg 1104
 Val Met Asp Ala Thr His Pro His His Tyr Phe Met Asp Asn Val Leu
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<400> 22

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 35 40 45

Gln Glu His Asp Gly Tyr Ala Tyr Gln Ser His His Gln Gln Ser Ser
 50 55 60

Ser Leu Phe Leu Gln Ser Leu Ala Pro Pro Gln Gly Thr Lys Asn Lys
 65 70 75 80

Val Ala Ser Ser Ser Ser Pro Ser Ser Cys Ala Pro Ala Tyr Ser Leu
 85 90 95

Met Glu Ile His His Asn Glu Ile Val Ala Gly Gly Ile Asn Pro Cys
 100 105 110

Ser Ser Phe Ser Ser Ser Ala Ser Val Lys Ala Lys Ile Met Ala His
 115 120 125

Pro His Tyr His Arg Leu Leu Ala Ala Tyr Val Asn Cys Gln Lys Val
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Gly Ala Pro Pro Glu Val Val Ala Arg Leu Glu Glu Ala Cys Ser Ser
 145 150 155 160

Ala Ala Ala Ala Ala Ala Ser Met Gly Pro Thr Gly Cys Leu Gly Glu
 165 170 175

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Asp Pro Gly Leu Asp Gln Phe Met Glu Ala Tyr Cys Glu Met Leu Val
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Lys Tyr Glu Gln Glu Leu Ser Lys Pro Phe Lys Glu Ala Met Val Phe
 195 200 205

Leu Gln Arg Val Glu Cys Gln Phe Lys Ser Leu Ser Leu Ser Ser Pro
 210 215 220

Ser Ser Phe Ser Gly Tyr Gly Glu Thr Ala Ile Asp Arg Asn Asn Asn
 225 230 235 240

Gly Ser Ser Glu Glu Glu Val Asp Met Asn Asn Glu Phe Val Asp Pro
 245 250 255

Gln Ala Glu Asp Arg Glu Leu Lys Gly Gln Leu Leu Arg Lys Tyr Ser
 260 265 270

Gly Tyr Leu Gly Ser Leu Lys Gln Glu Phe Met Lys Lys Arg Lys Lys
 275 280 285

Gly Lys Leu Pro Lys Glu Ala Arg Gln Gln Leu Leu Asp Trp Trp Ser
 290 295 300

Arg His Tyr Lys Trp Pro Tyr Pro Ser Glu Gln Gln Lys Leu Ala Leu
 305 310 315 320

Ala Glu Ser Thr Gly Leu Asp Gln Lys Gln Ile Asn Asn Trp Phe Ile
 325 330 335

Asn Gln Arg Lys Arg His Trp Lys Pro Ser Glu Asp Met Gln Phe Val
 340 345 350

Val Met Asp Ala Thr His Pro His His Tyr Phe Met Asp Asn Val Leu
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Asp Asn Pro Phe Pro Met Asp His Ile Ser Ser Thr Met Leu
 370 375 380

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 atg tct aat gaa acc aga gat ctc tac aac tac caa tac cct tca tcg 165
 Met Ser Asn Glu Thr Arg Asp Leu Tyr Asn Tyr Gln Tyr Pro Ser Ser
 1 5 10 15
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MBI0018 Sequence Listing.ST25

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tcg atc gat caa gaa ccg aac cgt gat gtt act aat gac gta atc aat Ser Ile Asp Gln Glu Pro Asn Arg Asp Val Thr Asn Asp Val Ile Asn 85 90 95	405
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1136

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Tyr Gly Asn Leu Pro Ser Gln Asn Gly Phe Asn Pro Ser Thr Tyr Ser
 35 40 45

Phe Thr Asp Cys Leu Gln Ser Ser Pro Ala Ala Tyr Glu Ser Leu Leu
 50 55 60

Gln Lys Thr Phe Gly Leu Ser Pro Ser Ser Ser Glu Val Phe Asn Ser
 65 70 75 80

Ser Ile Asp Gln Glu Pro Asn Arg Asp Val Thr Asn Asp Val Ile Asn
 85 90 95

Gly Gly Ala Cys Asn Glu Thr Glu Thr Arg Val Ser Pro Ser Asn Ser
 100 105 110

Ser Ser Ser Glu Ala Asp His Pro Gly Glu Asp Ser Gly Lys Ser Arg
 115 120 125

Arg Lys Arg Glu Leu Val Gly Glu Glu Asp Gln Ile Ser Lys Lys Val
 130 135 140

Gly Lys Thr Lys Lys Thr Glu Val Lys Lys Gln Arg Glu Pro Arg Val
 145 150 155 160

Ser Phe Met Thr Lys Ser Glu Val Asp His Leu Glu Asp Gly Tyr Arg
 165 170 175

Trp Arg Lys Tyr Gly Gln Lys Ala Val Lys Asn Ser Pro Tyr Pro Arg
 180 185 190

Ser Tyr Tyr Arg Cys Thr Thr Gln Lys Cys Asn Val Lys Lys Arg Val
 195 200 205

Glu Arg Ser Phe Gln Asp Pro Thr Val Val Ile Thr Thr Tyr Glu Gly
 210 215 220

Gln His Asn His Pro Ile Pro Thr Asn Leu Arg Gly Ser Ser Ala Ala
 225 230 235 240

Ala Ala Met Phe Ser Ala Asp Leu Met Thr Pro Arg Ser Phe Ala His
 245 250 255

Asp Met Phe Arg Thr Ala Ala Tyr Thr Asn Gly Gly Ser Val Ala Ala

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260 265 270

Ala Leu Asp Tyr Gly Tyr Gly Gln Ser Gly Tyr Gly Ser Val Asn Ser
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Asn Pro Ser Ser His Gln Val Tyr His Gln Gly Gly Glu Tyr Glu Leu
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Phe Ser Ser Ser Gly Phe Ser Asp Pro Lys Glu Thr Arg Asn Val Ser	
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gtc gcc ggc gag ggg caa aaa agt aat tct acc cga tcc gct gcg gct	144
Val Ala Gly Glu Gly Gln Lys Ser Asn Ser Thr Arg Ser Ala Ala Ala	
35 40 45	
gag cgt gct ttg gac cct gag gct gct ctt tac aga gag cta tgg cac	192
Glu Arg Ala Leu Asp Pro Glu Ala Ala Leu Tyr Arg Glu Leu Trp His	
50 55 60	
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Ala Cys Ala Gly Pro Leu Val Thr Val Pro Arg Gln Asp Asp Arg Val	
65 70 75 80	
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Phe Tyr Phe Pro Gln Gly His Ile Glu Gln Val Glu Ala Ser Thr Asn	
85 90 95	
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Gln Ala Ala Glu Gln Gln Met Pro Leu Tyr Asp Leu Pro Ser Lys Leu	
100 105 110	
ctc tgt cga gtt att aat gta gat tta aag gca gag gca gat aca gat	384
Leu Cys Arg Val Ile Asn Val Asp Leu Lys Ala Glu Ala Asp Thr Asp	
115 120 125	
gaa gtt tat gcg cag att act ctt ctt cct gag gct aat caa gac gag	432
Glu Val Tyr Ala Gln Ile Thr Leu Leu Pro Glu Ala Asn Gln Asp Glu	
130 135 140	
aat gca att gag aaa gaa gcg cct ctt cct cca cct ccg agg ttc cag	480
Asn Ala Ile Glu Lys Glu Ala Pro Leu Pro Pro Pro Arg Phe Gln	
145 150 155 160	
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Val His Ser Phe Cys Lys Thr Leu Thr Ala Ser Asp Thr Ser Thr His	
165 170 175	
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Gly Gly Phe Ser Val Leu Arg Arg His Ala Asp Glu Cys Leu Pro Pro	
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acc gca tgg cat gcc att tca aca ggg act atg ttt aca gtc tac tac Thr Ala Trp His Ala Ile Ser Thr Gly Thr Met Phe Thr Val Tyr Tyr 290 295 300	912
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aag gca aac atg gac cct tta cca gca agc gga ctt tca agg gtc ttg Lys Ala Asn Met Asp Pro Leu Pro Ala Ser Gly Leu Ser Arg Val Leu 435 440 445	1344
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gaa tat cct gtt ctt aat ggt cta tgc act gag aat gct ggt ggt aac Glu Tyr Pro Val Leu Asn Gly Leu Ser Thr Glu Asn Ala Gly Gly Asn 595 600 605	1824
tgg cca ata cgt cca cgt gct ttg aat tat tat gag gaa gtg gtc aat Trp Pro Ile Arg Pro Arg Ala Leu Asn Tyr Tyr Glu Glu Val Val Asn 610 615 620	1872
gct caa gcg caa gct cag gct agg gag caa gta aca aaa caa ccc ttc Ala Gln Ala Gln Ala Gln Ala Arg Glu Gln Val Thr Lys Gln Pro Phe 625 630 635 640	1920
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gag ttc aat gga gag ttg atg gct cct aag aaa gat tgg ttg ata gtt Glu Phe Asn Gly Glu Leu Met Ala Pro Lys Lys Asp Trp Leu Ile Val 770 775 780	2352
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gaa gtg agg aag atg aac ccg ggg act tta agc tgt agg agc gag gaa      2496
Glu Val Arg Lys Met Asn Pro Gly Thr Leu Ser Cys Arg Ser Glu Glu
      820      825      830

gaa gca gtt gtt ggg gaa gga tca gat gca aag gac gcc aag tct gca      2544
Glu Ala Val Val Gly Glu Gly Ser Asp Ala Lys Asp Ala Lys Ser Ala
      835      840      845

tca aat cct tca ttg tcc agc gct ggg aac tct taa      2580
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<210> 26
<211> 859
<212> PRT
<213> Arabidopsis thaliana

<400> 26

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20          25          30

Val Ala Gly Glu Gly Gln Lys Ser Asn Ser Thr Arg Ser Ala Ala Ala
35          40          45

Glu Arg Ala Leu Asp Pro Glu Ala Ala Leu Tyr Arg Glu Leu Trp His
50          55          60

Ala Cys Ala Gly Pro Leu Val Thr Val Pro Arg Gln Asp Asp Arg Val
65          70          75          80

Phe Tyr Phe Pro Gln Gly His Ile Glu Gln Val Glu Ala Ser Thr Asn
85          90          95

Gln Ala Ala Glu Gln Gln Met Pro Leu Tyr Asp Leu Pro Ser Lys Leu
100         105         110

Leu Cys Arg Val Ile Asn Val Asp Leu Lys Ala Glu Ala Asp Thr Asp
115         120         125

Glu Val Tyr Ala Gln Ile Thr Leu Leu Pro Glu Ala Asn Gln Asp Glu
130         135         140

Asn Ala Ile Glu Lys Glu Ala Pro Leu Pro Pro Pro Pro Arg Phe Gln
145         150         155         160

Val His Ser Phe Cys Lys Thr Leu Thr Ala Ser Asp Thr Ser Thr His
165         170         175

Gly Gly Phe Ser Val Leu Arg Arg His Ala Asp Glu Cys Leu Pro Pro
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Leu Asp Met Ser Arg Gln Pro Pro Thr Gln Glu Leu Val Ala Lys Asp

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200 205

195

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Arg Arg His Leu Leu Gln Ser Gly Trp Ser Val Phe Val Ser Ser Lys
225 230 235 240

Arg Leu Val Ala Gly Asp Ala Phe Ile Phe Leu Arg Gly Glu Asn Gly
245 250 255

Glu Leu Arg Val Gly Val Arg Arg Ala Met Arg Gln Gln Gly Asn Val
260 265 270

Pro Ser Ser Val Ile Ser Ser His Ser Met His Leu Gly Val Leu Ala
275 280 285

Thr Ala Trp His Ala Ile Ser Thr Gly Thr Met Phe Thr Val Tyr Tyr
290 295 300

Lys Pro Arg Thr Ser Pro Ser Glu Phe Ile Val Pro Phe Asp Gln Tyr
305 310 315 320

Met Glu Ser Val Lys Asn Asn Tyr Ser Ile Gly Met Arg Phe Lys Met
325 330 335

Arg Phe Glu Gly Glu Glu Ala Pro Glu Gln Arg Phe Thr Gly Thr Ile
340 345 350

Val Gly Ile Glu Glu Ser Asp Pro Thr Arg Trp Pro Lys Ser Lys Trp
355 360 365

Arg Ser Leu Lys Val Arg Trp Asp Glu Thr Ser Ser Ile Pro Arg Pro
370 375 380

Asp Arg Val Ser Pro Trp Lys Val Glu Pro Ala Leu Ala Pro Pro Ala
385 390 395 400

Leu Ser Pro Val Pro Met Pro Arg Pro Lys Arg Pro Arg Ser Asn Ile
405 410 415

Ala Pro Ser Ser Pro Asp Ser Ser Met Leu Thr Arg Glu Gly Thr Thr
420 425 430

Lys Ala Asn Met Asp Pro Leu Pro Ala Ser Gly Leu Ser Arg Val Leu
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Gln Gly Gln Glu Tyr Ser Thr Leu Arg Thr Lys His Thr Glu Ser Val
450 455 460

Glu Cys Asp Ala Pro Glu Asn Ser Val Val Trp Gln Ser Ser Ala Asp
465 470 475 480

Asp Asp Lys Val Asp Val Val Ser Gly Ser Arg Arg Tyr Gly Ser Glu
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MBI0018 Sequence Listing.ST25

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Ser Gly Phe Gly Thr Asn Ile Asp Pro Ser His Gly Gln Arg Ile Pro
 515 520 525

Phe Tyr Asp His Ser Ser Ser Pro Ser Met Pro Ala Lys Arg Ile Leu
 530 535 540

Ser Asp Ser Glu Gly Lys Phe Asp Tyr Leu Ala Asn Gln Trp Gln Met
 545 550 555 560

Ile His Ser Gly Leu Ser Leu Lys Leu His Glu Ser Pro Lys Val Pro
 565 570 575

Ala Ala Thr Asp Ala Ser Leu Gln Gly Arg Cys Asn Val Lys Tyr Ser
 580 585 590

Glu Tyr Pro Val Leu Asn Gly Leu Ser Thr Glu Asn Ala Gly Gly Asn
 595 600 605

Trp Pro Ile Arg Pro Arg Ala Leu Asn Tyr Tyr Glu Glu Val Val Asn
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Thr Ile Gln Glu Glu Thr Ala Lys Ser Arg Glu Gly Asn Cys Arg Leu
 645 650 655

Phe Gly Ile Pro Leu Thr Asn Asn Met Asn Gly Thr Asp Ser Thr Met
 660 665 670

Ser Gln Arg Asn Asn Leu Asn Asp Ala Ala Gly Leu Thr Gln Ile Ala
 675 680 685

Ser Pro Lys Val Gln Asp Leu Ser Asp Gln Ser Lys Gly Ser Lys Ser
 690 695 700

Thr Asn Asp His Arg Glu Gln Gly Arg Pro Phe Gln Thr Asn Asn Pro
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His Pro Lys Asp Ala Gln Thr Lys Thr Asn Ser Ser Arg Ser Cys Thr
 725 730 735

Lys Val His Lys Gln Gly Ile Ala Leu Gly Arg Ser Val Asp Leu Ser
 740 745 750

Lys Phe Gln Asn Tyr Glu Glu Leu Val Ala Glu Leu Asp Arg Leu Phe
 755 760 765

Glu Phe Asn Gly Glu Leu Met Ala Pro Lys Lys Asp Trp Leu Ile Val
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Tyr Thr Asp Glu Glu Asn Asp Met Met Leu Val Gly Asp Asp Pro Trp
 785 790 795 800

MBI0018 Sequence Listing.ST25

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805 810 815

Glu Val Arg Lys Met Asn Pro Gly Thr Leu Ser Cys Arg Ser Glu Glu
820 825 830

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850 855

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<223> G615

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cttcttaagt tcgggtg atg tcg tct tcc acc aat gac tac aac gat ggt aat 232
Met Ser Ser Ser Thr Asn Asp Tyr Asn Asp Gly Asn
1 5 10
aac aat gga gtg tac cct ctc tct ctt tac ctt tct tca ctc tct ggc 280
Asn Asn Gly Val Tyr Pro Leu Ser Leu Tyr Leu Ser Ser Leu Ser Gly
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His Gln Asp Ile Ile His Asn Pro Tyr Asn His Gln Leu Lys Ala Ser
30 35 40
ccg ggc cat atg gta tca gca gtt cct gaa tct ctg atc gat tac atg 376
Pro Gly His Met Val Ser Ala Val Pro Glu Ser Leu Ile Asp Tyr Met
45 50 55 60
gcg ttt aag tca aat aat gtt gtg aat caa caa ggc ttt gag ttt cct 424
Ala Phe Lys Ser Asn Asn Val Val Asn Gln Gln Gly Phe Glu Phe Pro
65 70 75
gag gtg tca aag gaa atc aag aag gtg gtg aag aag gac cga cat agc 472
Glu Val Ser Lys Glu Ile Lys Lys Val Val Lys Lys Asp Arg His Ser
80 85 90
aag att caa acg gca caa ggg att aga gac agg agg gtt agg ctt ttt 520
Lys Ile Gln Thr Ala Gln Gly Ile Arg Asp Arg Arg Val Arg Leu Phe
95 100 105
att ggg att gct cgc caa ttc ttt gat ctt cag gat atg ttg ggg ttt 568
Ile Gly Ile Ala Arg Gln Phe Phe Asp Leu Gln Asp Met Leu Gly Phe
110 115 120
gat aaa gct agt aaa acg tta gac tgg ctg ctc aag aag tca aga aaa 616
Asp Lys Ala Ser Lys Thr Leu Asp Trp Leu Leu Lys Lys Ser Arg Lys
125 130 135 140
gcc atc aaa gag gtc gta caa gca aaa aac ctc aac aat gat gat gaa 664
Ala Ile Lys Glu Val Val Gln Ala Lys Asn Leu Asn Asn Asp Asp Glu
145 150 155

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gat ttt gga aac att gga ggc gat gta gaa caa gaa gag gag aag gag      712
Asp Phe Gly Asn Ile Gly Gly Asp Val Glu Gln Glu Glu Lys Glu
      160      165      170

gag gat gac aat ggc gat aag agc ttc gtg tat ggt ttg agc ccc ggg      760
Glu Asp Asp Asn Gly Asp Lys Ser Phe Val Tyr Gly Leu Ser Pro Gly
      175      180      185

tac ggt gaa gaa gaa gtg gta tgt gag gcc acg aag gca ggg ata aga      808
Tyr Gly Glu Glu Glu Val Val Cys Glu Ala Thr Lys Ala Gly Ile Arg
      190      195      200

aag aag aag agt gag ttg aga aac atc tca tca aag ggg cta gga gcc      856
Lys Lys Lys Ser Glu Leu Arg Asn Ile Ser Ser Lys Gly Leu Gly Ala
      205      210      215      220

aaa gct aga gga aaa gca aag gag cga aca aaa gag atg atg gcc tat      904
Lys Ala Arg Gly Lys Ala Lys Glu Arg Thr Lys Glu Met Met Ala Tyr
      225      230      235

gat aat cca gag act gcc tct gat att aca caa tct gaa atc atg gac      952
Asp Asn Pro Glu Thr Ala Ser Asp Ile Thr Gln Ser Glu Ile Met Asp
      240      245      250

cca ttc aag agg tct ata gtc ttc aat gaa gga gaa gat atg aca cac      1000
Pro Phe Lys Arg Ser Ile Val Phe Asn Glu Gly Glu Asp Met Thr His
      255      260      265

ctt ttc tac aag gaa cca atc gag gag ttt gat aat caa gaa tct atc      1048
Leu Phe Tyr Lys Glu Pro Ile Glu Glu Phe Asp Asn Gln Glu Ser Ile
      270      275      280

tta acc aat atg act cta cca acg aag atg ggt caa agt tac aat caa      1096
Leu Thr Asn Met Thr Leu Pro Thr Lys Met Gly Gln Ser Tyr Asn Gln
      285      290      295      300

aat aat ggg ata ctt atg ttg gta gat cag agt tct agc agc aac tat      1144
Asn Asn Gly Ile Leu Met Leu Val Asp Gln Ser Ser Ser Ser Asn Tyr
      305      310      315

aat aca ttt ctg cct caa aat ttg gat tat agt tat gat caa aac cct      1192
Asn Thr Phe Leu Pro Gln Asn Leu Asp Tyr Ser Tyr Asp Gln Asn Pro
      320      325      330

ttt cat gac caa acc tta tat gta gtc acc gac aaa aat ttc ccc aaa      1240
Phe His Asp Gln Thr Leu Tyr Val Val Thr Asp Lys Asn Phe Pro Lys
      335      340      345

ggg ttc cta taa atctcgacag ttttgaagga ctatgcatga tcaagtttaa      1292
Gly Phe Leu
      350

acatgtaagc caatatagtc ccttattcct ctgaatgtat acaaaatcta tagttatgta      1352

tatctgttcc tttttaacgt atctttattg atcttctgtg ccttgatcaa aattgtcatt      1412

ttaagattca gtttgtgtaa tattttagct acaactttta agtggtatta ttgtaacctt      1472

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Ile His Asn Pro Tyr Asn His Gln Leu Lys Ala Ser Pro Gly His Met
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 Val Ser Ala Val Pro Glu Ser Leu Ile Asp Tyr Met Ala Phe Lys Ser
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 Asn Asn Val Val Asn Gln Gln Gly Phe Glu Phe Pro Glu Val Ser Lys
 65 70 75 80
 Glu Ile Lys Lys Val Val Lys Lys Asp Arg His Ser Lys Ile Gln Thr
 85 90 95
 Ala Gln Gly Ile Arg Asp Arg Arg Val Arg Leu Phe Ile Gly Ile Ala
 100 105 110
 Arg Gln Phe Phe Asp Leu Gln Asp Met Leu Gly Phe Asp Lys Ala Ser
 115 120 125
 Lys Thr Leu Asp Trp Leu Leu Lys Lys Ser Arg Lys Ala Ile Lys Glu
 130 135 140
 Val Val Gln Ala Lys Asn Leu Asn Asn Asp Asp Glu Asp Phe Gly Asn
 145 150 155 160
 Ile Gly Gly Asp Val Glu Gln Glu Glu Glu Lys Glu Glu Asp Asp Asn
 165 170 175
 Gly Asp Lys Ser Phe Val Tyr Gly Leu Ser Pro Gly Tyr Gly Glu Glu
 180 185 190
 Glu Val Val Cys Glu Ala Thr Lys Ala Gly Ile Arg Lys Lys Lys Ser
 195 200 205
 Glu Leu Arg Asn Ile Ser Ser Lys Gly Leu Gly Ala Lys Ala Arg Gly
 210 215 220
 Lys Ala Lys Glu Arg Thr Lys Glu Met Met Ala Tyr Asp Asn Pro Glu
 225 230 235 240
 Thr Ala Ser Asp Ile Thr Gln Ser Glu Ile Met Asp Pro Phe Lys Arg
 245 250 255
 Ser Ile Val Phe Asn Glu Gly Glu Asp Met Thr His Leu Phe Tyr Lys
 260 265 270
 Glu Pro Ile Glu Glu Phe Asp Asn Gln Glu Ser Ile Leu Thr Asn Met
 275 280 285
 Thr Leu Pro Thr Lys Met Gly Gln Ser Tyr Asn Gln Asn Asn Gly Ile
 290 295 300
 Leu Met Leu Val Asp Gln Ser Ser Ser Ser Asn Tyr Asn Thr Phe Leu
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 Pro Gln Asn Leu Asp Tyr Ser Tyr Asp Gln Asn Pro Phe His Asp Gln
 325 330 335

MBI0018 Sequence Listing.ST25

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 Met Glu Leu Asn Arg Ser Glu Ala Asp Glu Ala Lys Ala Glu Thr Thr
 1 5 10 15
 ccc acc ggt gga gcc acc agc tca gcc aca gcc tct ggc tct tcc tcc 157
 Pro Thr Gly Gly Ala Thr Ser Ser Ala Thr Ala Ser Gly Ser Ser Ser
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 gga cgt cgt cca cgt ggt cgt cct gca ggt tcc aaa aac aaa ccc aaa 205
 Gly Arg Arg Pro Arg Gly Arg Pro Ala Gly Ser Lys Asn Lys Pro Lys
 35 40 45
 cct ccg acg att ata act aga gat agt cct aac gtc ctt aga tca cac 253
 Pro Pro Thr Ile Ile Thr Arg Asp Ser Pro Asn Val Leu Arg Ser His
 50 55 60
 gtt ctt gaa gtc acc tcc ggt tcg gac ata tcc gag gca gtc tcc acc 301
 Val Leu Glu Val Thr Ser Gly Ser Asp Ile Ser Glu Ala Val Ser Thr
 65 70 75 80
 tac gcc act cgt cgc ggc tgc ggc gtt tgc att ata agc ggc acg ggt 349
 Tyr Ala Thr Arg Arg Gly Cys Gly Val Cys Ile Ile Ser Gly Thr Gly
 85 90 95
 gcg gtc act aac gtc acg ata cgg caa cct gcg gct ccg gct ggt gga 397
 Ala Val Thr Asn Val Thr Ile Arg Gln Pro Ala Ala Pro Ala Gly Gly
 100 105 110
 ggt gtg att acc ctg cat ggt cgg ttt gac att ttg tct ttg acc ggt 445
 Gly Val Ile Thr Leu His Gly Arg Phe Asp Ile Leu Ser Leu Thr Gly
 115 120 125
 act gcg ctt cca ccg cct gca cca ccg gga gca gga ggt ttg acg gtg 493
 Thr Ala Leu Pro Pro Pro Ala Pro Pro Gly Ala Gly Gly Leu Thr Val
 130 135 140
 tat cta gcc gga ggt caa gga caa gtt gta gga ggg aat gtg gct ggt 541
 Tyr Leu Ala Gly Gly Gln Gly Gln Val Val Gly Gly Asn Val Ala Gly
 145 150 155 160
 tcg tta att gct tcg gga ccg gta gtg ttg atg gct gct tct ttt gca 589
 Ser Leu Ile Ala Ser Gly Pro Val Val Leu Met Ala Ala Ser Phe Ala
 165 170 175
 aac gca gtt tat gat agg tta ccg att gaa gag gaa gaa acc cca ccg 637
 Asn Ala Val Tyr Asp Arg Leu Pro Ile Glu Glu Glu Glu Thr Pro Pro
 180 185 190
 ccg aga acc acc ggg gtg cag cag cag cag ccg gag gcg tct cag tcg 685
 Pro Arg Thr Thr Gly Val Gln Gln Gln Gln Pro Glu Ala Ser Gln Ser
 195 200 205
 tcg gag gtt acg ggg agt ggg gcc cag gcg tgt gag tca aac ctc caa 733
 Ser Glu Val Thr Gly Ser Gly Ala Gln Ala Cys Glu Ser Asn Leu Gln
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MBI0018 Sequence Listing.ST25

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atg aac aat ttt caa ttc tcc ggg gga gat att tac ggt atg agc ggc      829
Met Asn Asn Phe Gln Phe Ser Gly Gly Asp Ile Tyr Gly Met Ser Gly
                245                250                255

ggg agc gga gga ggt ggt ggc ggt gcg act aga ccc gcg ttt tag      874
Gly Ser Gly Gly Gly Gly Gly Gly Ala Thr Arg Pro Ala Phe
                260                265                270

agtttttagcg ttttggtgac accttttggt gcgtttgcgt gtttgacctc aaactactag      934

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35                40                45

Pro Pro Thr Ile Ile Thr Arg Asp Ser Pro Asn Val Leu Arg Ser His
50                55                60

Val Leu Glu Val Thr Ser Gly Ser Asp Ile Ser Glu Ala Val Ser Thr
65                70                75                80

Tyr Ala Thr Arg Arg Gly Cys Gly Val Cys Ile Ile Ser Gly Thr Gly
85                90                95

Ala Val Thr Asn Val Thr Ile Arg Gln Pro Ala Ala Pro Ala Gly Gly
100                105                110

Gly Val Ile Thr Leu His Gly Arg Phe Asp Ile Leu Ser Leu Thr Gly
115                120                125

Thr Ala Leu Pro Pro Pro Ala Pro Pro Gly Ala Gly Gly Leu Thr Val
130                135                140

Tyr Leu Ala Gly Gly Gln Gly Gln Val Val Gly Gly Asn Val Ala Gly
145                150                155                160

Ser Leu Ile Ala Ser Gly Pro Val Val Leu Met Ala Ala Ser Phe Ala
165                170                175

Asn Ala Val Tyr Asp Arg Leu Pro Ile Glu Glu Glu Glu Thr Pro Pro
180                185                190

Pro Arg Thr Thr Gly Val Gln Gln Gln Gln Pro Glu Ala Ser Gln Ser
195                200                205

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MBI0018 Sequence Listing.ST25

Ser Glu Val Thr Gly Ser Gly Ala Gln Ala Cys Glu Ser Asn Leu Gln
210 215 220

Gly Gly Asn Gly Gly Gly Gly Val Ala Phe Tyr Asn Leu Gly Met Asn
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Met Asn Asn Phe Gln Phe Ser Gly Gly Asp Ile Tyr Gly Met Ser Gly
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Ser Ser Gly Arg Asn Gln Gly Gly Gly Gly Glu Thr Val Val Glu Met
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ttt cct tct ggt ctt cga gtt ctt gtc gtt gac gat gac cca act tgt 144
Phe Pro Ser Gly Leu Arg Val Leu Val Val Asp Asp Pro Thr Cys
35 40 45
ctc atg atc tta gag agg atg ctt agg act tgt ctt tac gaa gta acg 192
Leu Met Ile Leu Glu Arg Met Leu Arg Thr Cys Leu Tyr Glu Val Thr
50 55 60
aaa tgc aac aga gca gag atg gca ttg tct ctg ctc cgg aag aac aaa 240
Lys Cys Asn Arg Ala Glu Met Ala Leu Ser Leu Leu Arg Lys Asn Lys
65 70 75 80
cat gga ttc gat ata gta atc agt gat gtt cat atg cct gac atg gac 288
His Gly Phe Asp Ile Val Ile Ser Asp Val His Met Pro Asp Met Asp
85 90 95
ggt ttc aag ctt ctt gag cat gtt ggt cta gag atg gac tta cct gtt 336
Gly Phe Lys Leu Leu Glu His Val Gly Leu Glu Met Asp Leu Pro Val
100 105 110
atc atg atg tct gcg gat gat tca aag agt gtg gtt cta aag gga gta 384
Ile Met Met Ser Ala Asp Asp Ser Lys Ser Val Val Leu Lys Gly Val
115 120 125
acg cac ggt gcg gtt gat tac ctt atc aag cct gta cgt atg gag gca 432
Thr His Gly Ala Val Asp Tyr Leu Ile Lys Pro Val Arg Met Glu Ala
130 135 140
ctt aag aac ata tgg cag cat gta gtt agg aag agg aga agt gaa tgg 480
Leu Lys Asn Ile Trp Gln His Val Val Arg Lys Arg Arg Ser Glu Trp
145 150 155 160
agt gta ccg gaa cat tct ggg agc att gag gag act ggc gag aga cag 528
Ser Val Pro Glu His Ser Gly Ser Ile Glu Glu Thr Gly Glu Arg Gln
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MBI0018 Sequence Listing.ST25

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gag	gat	gcg	gtg	gat	gat	aac	tca	tcc	tcg	gtt	aac	gaa	ggt	aac	aat	624
Glu	Asp	Ala	Val	Asp	Asp	Asn	Ser	Ser	Ser	Val	Asn	Glu	Gly	Asn	Asn	
195							200					205				
tgg	agg	agc	agt	tca	cgg	aag	agg	aaa	gac	gag	gaa	gga	gaa	gag	caa	672
Trp	Arg	Ser	Ser	Ser	Arg	Lys	Arg	Lys	Asp	Glu	Glu	Gly	Glu	Glu	Gln	
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Gly	Asp	Asp	Lys	Asp	Glu	Asp	Ala	Ser	Asn	Leu	Lys	Lys	Pro	Arg	Val	
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gtc	tgg	tct	gtt	gaa	ttg	cat	cag	cag	ttt	gtt	gct	gct	gtt	aat	cag	768
Val	Trp	Ser	Val	Glu	Leu	His	Gln	Gln	Phe	Val	Ala	Ala	Val	Asn	Gln	
			245						250					255		
ctc	ggc	gtt	gag	aag	gcg	gtt	cct	aaa	aag	atc	tta	gag	ctg	atg	aat	816
Leu	Gly	Val	Glu	Lys	Ala	Val	Pro	Lys	Lys	Ile	Leu	Glu	Leu	Met	Asn	
			260					265					270			
gtt	cct	ggt	cta	acc	cga	gaa	aac	gta	gca	agt	cac	ctc	cag	aaa	tac	864
Val	Pro	Gly	Leu	Thr	Arg	Glu	Asn	Val	Ala	Ser	His	Leu	Gln	Lys	Tyr	
		275					280					285				
cgg	ata	tat	cta	aga	cgg	ctt	gga	ggg	gta	tcg	cag	cac	caa	ggc	aat	912
Arg	Ile	Tyr	Leu	Arg	Arg	Leu	Gly	Gly	Val	Ser	Gln	His	Gln	Gly	Asn	
	290					295					300					
ctt	aac	aac	tcg	ttt	atg	acg	ggt	cag	gat	gcg	agc	ttc	gga	cct	ctt	960
Leu	Asn	Asn	Ser	Phe	Met	Thr	Gly	Gln	Asp	Ala	Ser	Phe	Gly	Pro	Leu	
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tcg	aca	ttg	aat	ggg	ttt	gat	ctt	caa	gca	cta	gcc	gtc	aca	ggt	cag	1008
Ser	Thr	Leu	Asn	Gly	Phe	Asp	Leu	Gln	Ala	Leu	Ala	Val	Thr	Gly	Gln	
				325					330					335		
tta	cct	gca	cag	agt	ctt	gca	cag	ctt	caa	gcc	gct	ggt	tta	ggc	cgg	1056
Leu	Pro	Ala	Gln	Ser	Leu	Ala	Gln	Leu	Gln	Ala	Ala	Gly	Leu	Gly	Arg	
			340					345					350			
cct	gcg	atg	gtc	tct	aag	tca	ggt	ttg	ccg	gtt	tcc	tcc	att	gtg	gat	1104
Pro	Ala	Met	Val	Ser	Lys	Ser	Gly	Leu	Pro	Val	Ser	Ser	Ile	Val	Asp	
		355					360					365				
gag	aga	agc	atc	ttc	agc	ttt	gac	aac	acg	aaa	aca	aga	ttt	gga	gaa	1152
Glu	Arg	Ser	Ile	Phe	Ser	Phe	Asp	Asn	Thr	Lys	Thr	Arg	Phe	Gly	Glu	
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ggg	ctt	ggg	cat	cac	ggg	caa	caa	ccc	caa	cag	caa	cca	cag	atg	aac	1200
Gly	Leu	Gly	His	His	Gly	Gln	Gln	Pro	Gln	Gln	Gln	Pro	Gln	Met	Asn	
					390				395					400		
tta	ctt	cac	ggt	gtc	ccc	acg	ggt	tta	caa	cag	cag	ctt	cct	atg	ggt	1248
Leu	Leu	His	Gly	Val	Pro	Thr	Gly	Leu	Gln	Gln	Gln	Leu	Pro	Met	Gly	
				405					410					415		
aat	cga	atg	agt	att	caa	caa	cag	att	gct	gct	gtt	cga	gct	gga	aat	1296
Asn	Arg	Met	Ser	Ile	Gln	Gln	Gln	Ile	Ala	Ala	Val	Arg	Ala	Gly	Asn	
			420					425					430			
agt	gtt	caa	aac	aac	gga	atg	ctg	atg	cct	cta	gcg	ggt	cag	cag	tct	1344
Ser	Val	Gln	Asn	Asn	Gly	Met	Leu	Met	Pro	Leu	Ala	Gly	Gln	Gln	Ser	
			435				440					445				
ttg	cct	cgg	gga	cca	ccg	cct	atg	cta	acc	tct	tcg	caa	tca	tcc	atc	1392
Leu	Pro	Arg	Gly	Pro	Pro	Pro	Met	Leu	Thr	Ser	Ser	Gln	Ser	Ser	Ile	
			450				455					460				
agg	cag	ccg	atg	tta	tca	aac	cgc	att	tcc	gag	aga	agt	ggt	ttc	tct	1440
Arg	Gln	Pro	Met	Leu	Ser	Asn	Arg	Ile	Ser	Glu	Arg	Ser	Gly	Phe	Ser	
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MBI0018 Sequence Listing.ST25

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act aat ctc aca aca caa cac tca tca agc tcg atg cct tat aac aac 1536
 Thr Asn Leu Thr Thr Gln His Ser Ser Ser Met Pro Tyr Asn Asn
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ttc caa cca gaa ctt ccc gtg aac agt ttc ccg ctg gca agt gca cca 1584
 Phe Gln Pro Glu Leu Pro Val Arg Lys Ala Ser Phe Pro Leu Ala Ser Ala Pro
 515 520 525

ggg ata tca gta ccg gtt cgg aaa gcc act tct tac cag gaa gag gtt 1632
 Gly Ile Ser Val Pro Val Arg Lys Ala Thr Ser Tyr Gln Glu Glu Val
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aac agc tcc gaa gcg ggt ttc att acg ccg agc tac gac atg ttc acc 1680
 Asn Ser Ser Glu Ala Gly Phe Ile Thr Pro Ser Tyr Asp Met Phe Thr
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acc aga cag aat gat tgg gat ctg agg aat att gga ata gcc ttt gac 1728
 Thr Arg Gln Asn Asp Trp Asp Leu Arg Asn Ile Gly Ile Ala Phe Asp
 565 570 575

tca cat cag gac tca gaa tcc gct gcg ttt tcc gct tca gaa gcc tac 1776
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 580 585 590

tct tct tcg tcc atg tca aga cac aac acg aca gtt gca gcc acc gag 1824
 Ser Ser Ser Ser Met Ser Arg His Asn Thr Thr Val Ala Ala Thr Glu
 595 600 605

cat ggc cga aac cac cag cag cca cca tcg gga atg gta cag cac cat 1872
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cag gtt tat gca gac gga aac ggt ggt tca gtg agg gtg aaa tca gag 1920
 Gln Val Tyr Ala Asp Gly Asn Gly Gly Ser Val Arg Val Lys Ser Glu
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aga gtg gct acg gat aca gca aca atg gcg ttt cac gag cag tat agt 1968
 Arg Val Ala Thr Asp Thr Ala Thr Met Ala Phe His Glu Gln Tyr Ser
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<400> 32

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Phe Pro Ser Gly Leu Arg Val Leu Val Val Asp Asp Asp Pro Thr Cys
 35 40 45

Leu Met Ile Leu Glu Arg Met Leu Arg Thr Cys Leu Tyr Glu Val Thr
 50 55 60

Lys Cys Asn Arg Ala Glu Met Ala Leu Ser Leu Leu Arg Lys Asn Lys
 65 70 75 80

MBI0018 Sequence Listing.ST25

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 Gly Phe Lys Leu Leu Glu His Val Gly Leu Glu Met Asp Leu Pro Val
 100 105 110
 Ile Met Met Ser Ala Asp Asp Ser Lys Ser Val Val Leu Lys Gly Val
 115 120 125
 Thr His Gly Ala Val Asp Tyr Leu Ile Lys Pro Val Arg Met Glu Ala
 130 135 140
 Leu Lys Asn Ile Trp Gln His Val Val Arg Lys Arg Arg Ser Glu Trp
 145 150 155 160
 Ser Val Pro Glu His Ser Gly Ser Ile Glu Glu Thr Gly Glu Arg Gln
 165 170 175
 Gln Gln Gln His Arg Gly Gly Gly Gly Gly Ala Ala Val Ser Gly Gly
 180 185 190
 Glu Asp Ala Val Asp Asp Asn Ser Ser Ser Val Asn Glu Gly Asn Asn
 195 200 205
 Trp Arg Ser Ser Ser Arg Lys Arg Lys Asp Glu Glu Gly Glu Glu Gln
 210 215 220
 Gly Asp Asp Lys Asp Glu Asp Ala Ser Asn Leu Lys Lys Pro Arg Val
 225 230 235 240
 Val Trp Ser Val Glu Leu His Gln Gln Phe Val Ala Ala Val Asn Gln
 245 250 255
 Leu Gly Val Glu Lys Ala Val Pro Lys Lys Ile Leu Glu Leu Met Asn
 260 265 270
 Val Pro Gly Leu Thr Arg Glu Asn Val Ala Ser His Leu Gln Lys Tyr
 275 280 285
 Arg Ile Tyr Leu Arg Arg Leu Gly Gly Val Ser Gln His Gln Gly Asn
 290 295 300
 Leu Asn Asn Ser Phe Met Thr Gly Gln Asp Ala Ser Phe Gly Pro Leu
 305 310 315 320
 Ser Thr Leu Asn Gly Phe Asp Leu Gln Ala Leu Ala Val Thr Gly Gln
 325 330 335
 Leu Pro Ala Gln Ser Leu Ala Gln Leu Gln Ala Ala Gly Leu Gly Arg
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 Pro Ala Met Val Ser Lys Ser Gly Leu Pro Val Ser Ser Ile Val Asp
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 Glu Arg Ser Ile Phe Ser Phe Asp Asn Thr Lys Thr Arg Phe Gly Glu
 370 375 380

MBI0018 Sequence Listing.ST25

Gly Leu Gly His His Gly Gln Gln Pro Gln Gln Gln Pro Gln Met Asn
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Leu Leu His Gly Val Pro Thr Gly Leu Gln Gln Gln Leu Pro Met Gly
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Asn Arg Met Ser Ile Gln Gln Gln Ile Ala Ala Val Arg Ala Gly Asn
420 425 430

Ser Val Gln Asn Asn Gly Met Leu Met Pro Leu Ala Gly Gln Gln Ser
435 440 445

Leu Pro Arg Gly Pro Pro Pro Met Leu Thr Ser Ser Gln Ser Ser Ile
450 455 460

Arg Gln Pro Met Leu Ser Asn Arg Ile Ser Glu Arg Ser Gly Phe Ser
465 470 475 480

Gly Arg Asn Asn Ile Pro Glu Ser Ser Arg Val Leu Pro Thr Ser Tyr
485 490 495

Thr Asn Leu Thr Thr Gln His Ser Ser Ser Ser Met Pro Tyr Asn Asn
500 505 510

Phe Gln Pro Glu Leu Pro Val Asn Ser Phe Pro Leu Ala Ser Ala Pro
515 520 525

Gly Ile Ser Val Pro Val Arg Lys Ala Thr Ser Tyr Gln Glu Glu Val
530 535 540

Asn Ser Ser Glu Ala Gly Phe Ile Thr Pro Ser Tyr Asp Met Phe Thr
545 550 555 560

Thr Arg Gln Asn Asp Trp Asp Leu Arg Asn Ile Gly Ile Ala Phe Asp
565 570 575

Ser His Gln Asp Ser Glu Ser Ala Ala Phe Ser Ala Ser Glu Ala Tyr
580 585 590

Ser Ser Ser Ser Met Ser Arg His Asn Thr Thr Val Ala Ala Thr Glu
595 600 605

His Gly Arg Asn His Gln Gln Pro Pro Ser Gly Met Val Gln His His
610 615 620

Gln Val Tyr Ala Asp Gly Asn Gly Gly Ser Val Arg Val Lys Ser Glu
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<213> Arabidopsis thaliana

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<222> (6)..(1091)
<223> G993

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      Met Glu Tyr Ser Cys Val Asp Asp Ser Ser Thr Thr Ser Glu Ser
      1          5          10          15

ctc tcc atc tct act act cca aag ccg aca acg acg acg gag aag aaa 98
Leu Ser Ile Ser Thr Thr Pro Lys Pro Thr Thr Thr Thr Glu Lys Lys
      20          25          30

ctc tct tct ccg ccg gcg acg tcg atg cgt ctc tac aga atg gga agc 146
Leu Ser Ser Pro Pro Ala Thr Ser Met Arg Leu Tyr Arg Met Gly Ser
      35          40          45

ggc gga agc agc gtc gtt ttg gat tca gag aac ggc gtc gag acc gag 194
Gly Gly Ser Ser Val Val Leu Asp Ser Glu Asn Gly Val Glu Thr Glu
      50          55          60

tca cgt aag ctt cct tcg tcg aaa tat aaa ggc gtt gtg cct cag cct 242
Ser Arg Lys Leu Pro Ser Ser Lys Tyr Lys Gly Val Val Pro Gln Pro
      65          70          75

aac gga aga tgg gga gct cag att tac gag aag cat cag cga gtt tgg 290
Asn Gly Arg Trp Gly Ala Gln Ile Tyr Glu Lys His Gln Arg Val Trp
      80          85          90

ctc ggt act ttc aac gag gaa gaa gaa gct gcg tct tct tac gac atc 338
Leu Gly Thr Phe Asn Glu Glu Glu Glu Ala Ala Ser Ser Tyr Asp Ile
      100          105          110

gcc gtg agg aga ttc cgc ggc cgc gac gcc gtc act aac ttc aaa tct 386
Ala Val Arg Arg Phe Arg Gly Arg Asp Ala Val Thr Asn Phe Lys Ser
      115          120          125

caa gtt gat gga aac gac gcc gaa tcg gct ttt ctt gac gct cat tct 434
Gln Val Asp Gly Asn Asp Ala Glu Ser Ala Phe Leu Asp Ala His Ser
      130          135          140

aaa gct gag atc gtg gat atg ttg agg aaa cac act tac gcc gat gag 482
Lys Ala Glu Ile Val Asp Met Leu Arg Lys His Thr Tyr Ala Asp Glu
      145          150          155

ttt gag cag agt aga cgg aag ttt gtt aac ggc gac gga aaa cgc tct 530
Phe Glu Gln Ser Arg Arg Lys Phe Val Asn Gly Asp Gly Lys Arg Ser
      160          165          170

ggg ttg gag acg gcg acg tac gga aac gac gct gtt ttg aga gcg cgt 578
Gly Leu Glu Thr Ala Thr Tyr Gly Asn Asp Ala Val Leu Arg Ala Arg
      180          185          190

gag gtt ttg ttc gag aag act gtt acg ccg agc gac gtc ggg aag ctg 626
Glu Val Leu Phe Glu Lys Thr Val Thr Pro Ser Asp Val Gly Lys Leu
      195          200          205

aac cgt tta gtg ata ccg aaa caa cac gcg gag aag cat ttt ccg tta 674
Asn Arg Leu Val Ile Pro Lys Gln His Ala Glu Lys His Phe Pro Leu
      210          215          220

ccg gcg atg acg acg gcg atg ggg atg aat ccg tct ccg acg aaa ggc 722
Pro Ala Met Thr Thr Ala Met Gly Met Asn Pro Ser Pro Thr Lys Gly
      225          230          235

gtt ttg att aac ttg gaa gat aga aca ggg aaa gtg tgg cgg ttc cgt 770
Val Leu Ile Asn Leu Glu Asp Arg Thr Gly Lys Val Trp Arg Phe Arg
      240          245          250

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MBI0018 Sequence Listing.ST25

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tac agt tac tgg aac agc agt caa agt tac gtg ttg acc aag ggc tgg      818
Tyr Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val Leu Thr Lys Gly Trp
                260                265                270

agc cgg ttc gtt aaa gag aag aat ctt cga gcc ggt gat gtg gtt tgt      866
Ser Arg Phe Val Lys Glu Lys Asn Leu Arg Ala Gly Asp Val Val Cys
                275                280                285

ttc gag aga tca acc gga cca gac cgg caa ttg tat atc cac tgg aaa      914
Phe Glu Arg Ser Thr Gly Pro Asp Arg Gln Leu Tyr Ile His Trp Lys
                290                295                300

gtc cgg tct agt ccg gtt cag act gtg gtt agg cta ttc gga gtc aac      962
Val Arg Ser Ser Pro Val Gln Thr Val Val Arg Leu Phe Gly Val Asn
                305                310                315

att ttc aat gtg agt aac gag aaa cca aac gac gtc gca gta gag tgt      1010
Ile Phe Asn Val Ser Asn Glu Lys Pro Asn Asp Val Ala Val Glu Cys
                320                325                330

gtt ggc aag aag aga tct cgg gaa gat gat ttg ttt tcg tta ggg tgt      1058
Val Gly Lys Lys Arg Ser Arg Glu Asp Asp Leu Phe Ser Leu Gly Cys
                340                345                350

tcc aag aag cag gcg att atc aac atc ttg tga caaattcttt ttttttggtt    1111
Ser Lys Lys Gln Ala Ile Ile Asn Ile Leu
                355                360

ttttttttca atttgtttct ccttttttcaa tattttgtat tgaaatgaca agttgtaa    1171
taggacaaga caagaaaaaa tgacaactag acaaaatagt ttttgtttaa aaaaaaaaaa    1231
aaaaaaaaa                                                                1239

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<210> 34
<211> 361
<212> PRT
<213> Arabidopsis thaliana

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<400> 34

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Ser Ile Ser Thr Thr Pro Lys Pro Thr Thr Thr Thr Glu Lys Lys Leu
20          25          30

Ser Ser Pro Pro Ala Thr Ser Met Arg Leu Tyr Arg Met Gly Ser Gly
35          40          45

Gly Ser Ser Val Val Leu Asp Ser Glu Asn Gly Val Glu Thr Glu Ser
50          55          60

Arg Lys Leu Pro Ser Ser Lys Tyr Lys Gly Val Val Pro Gln Pro Asn
65          70          75          80

Gly Arg Trp Gly Ala Gln Ile Tyr Glu Lys His Gln Arg Val Trp Leu
85          90          95

Gly Thr Phe Asn Glu Glu Glu Glu Ala Ala Ser Ser Tyr Asp Ile Ala
100         105         110

Val Arg Arg Phe Arg Gly Arg Asp Ala Val Thr Asn Phe Lys Ser Gln
115         120         125

Val Asp Gly Asn Asp Ala Glu Ser Ala Phe Leu Asp Ala His Ser Lys

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MBI0018 Sequence Listing.ST25

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130
135
140
Ala Glu Ile Val Asp Met Leu Arg Lys His Thr Tyr Ala Asp Glu Phe
145          150          155          160

Glu Gln Ser Arg Arg Lys Phe Val Asn Gly Asp Gly Lys Arg Ser Gly
165          170          175

Leu Glu Thr Ala Thr Tyr Gly Asn Asp Ala Val Leu Arg Ala Arg Glu
180          185          190

Val Leu Phe Glu Lys Thr Val Thr Pro Ser Asp Val Gly Lys Leu Asn
195          200          205

Arg Leu Val Ile Pro Lys Gln His Ala Glu Lys His Phe Pro Leu Pro
210          215          220

Ala Met Thr Thr Ala Met Gly Met Asn Pro Ser Pro Thr Lys Gly Val
225          230          235          240

Leu Ile Asn Leu Glu Asp Arg Thr Gly Lys Val Trp Arg Phe Arg Tyr
245          250          255

Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val Leu Thr Lys Gly Trp Ser
260          265          270

Arg Phe Val Lys Glu Lys Asn Leu Arg Ala Gly Asp Val Val Cys Phe
275          280          285

Glu Arg Ser Thr Gly Pro Asp Arg Gln Leu Tyr Ile His Trp Lys Val
290          295          300

Arg Ser Ser Pro Val Gln Thr Val Val Arg Leu Phe Gly Val Asn Ile
305          310          315          320

Phe Asn Val Ser Asn Glu Lys Pro Asn Asp Val Ala Val Glu Cys Val
325          330          335

Gly Lys Lys Arg Ser Arg Glu Asp Asp Leu Phe Ser Leu Gly Cys Ser
340          345          350

Lys Lys Gln Ala Ile Ile Asn Ile Leu
355          360

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<212> DNA
<213> Arabidopsis thaliana

<220>
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<222> (64)..(1098)
<223> G867

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taa atg gaa tcg agt agc gtt gat gag agt act aca agt aca ggt tcc 108
Met Glu Ser Ser Ser Val Asp Glu Ser Thr Thr Ser Thr Gly Ser

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MBI0018 Sequence Listing.ST25

1	5	10	15	
atc tgt gaa acc cgc gcg ata act ccg gcg aaa aag tcg tcg gta ggt				156
Ile Cys Glu Thr Pro Ala Ile Thr Pro Ala Lys Lys Ser Ser Val Gly	20	25	30	
aac tta tac agg atg gga agc gga tca agc gtt gtg tta gat tca gag				204
Asn Leu Tyr Arg Met Gly Ser Gly Ser Ser Val Val Leu Asp Ser Glu	35	40	45	
aac ggc gta gaa gct gaa tct agg aag ctt ccg tcg tca aaa tac aaa				252
Asn Gly Val Glu Ala Glu Ser Arg Lys Leu Pro Ser Ser Lys Tyr Lys	50	55	60	
ggg gtg gtc cca caa cca aac gga aga tgg gga gct cag att tac gag				300
Gly Val Val Pro Gln Pro Asn Gly Arg Trp Gly Ala Gln Ile Tyr Glu	65	70	75	
aaa cac cag cgc gtg tgg ctc ggg aca ttc aac gaa gaa gac gaa gcc				348
Lys His Gln Arg Val Trp Leu Gly Thr Phe Asn Glu Glu Asp Glu Ala	80	85	90	95
gct cgt gcc tac gac gtc gcg gtt cac agg ttc cgt cgc cgt gac gcc				396
Ala Arg Ala Tyr Asp Val Ala Val His Arg Phe Arg Arg Arg Asp Ala	100	105	110	
gtc aca aat ttc aaa gac gtg aag atg gac gaa gac gag gtc gat ttc				444
Val Thr Asn Phe Lys Asp Val Lys Met Asp Glu Asp Glu Val Asp Phe	115	120	125	
ttg aat tct cat tcg aaa tct gag atc gtt gat atg ttg agg aaa cat				492
Leu Asn Ser His Ser Lys Ser Glu Ile Val Asp Met Leu Arg Lys His	130	135	140	
act tat aac gaa gag tta gag cag agt aaa cgg cgt cgt aat ggt aac				540
Thr Tyr Asn Glu Glu Leu Glu Gln Ser Lys Arg Arg Arg Asn Gly Asn	145	150	155	
gga aac atg act agg acg ttg tta acg tcg ggg ttg agt aat gat ggt				588
Gly Asn Met Thr Arg Thr Leu Leu Thr Ser Gly Leu Ser Asn Asp Gly	160	165	170	175
gtt tct acg acg ggg ttt aga tcg gcg gag gca ctg ttt gag aaa gcg				636
Val Ser Thr Thr Phe Arg Ser Ala Glu Ala Leu Phe Glu Lys Ala	180	185	190	
gta acg cca agc gac gtt ggg aag cta aac cgt ttg gtt ata ccg aaa				684
Val Thr Pro Ser Asp Val Gly Lys Leu Asn Arg Leu Val Ile Pro Lys	195	200	205	
cat cac gca gag aaa cat ttt ccg tta ccg tca agt aac gtt tcc gtg				732
His His Ala Glu Lys His Phe Pro Leu Pro Ser Ser Asn Val Ser Val	210	215	220	
aaa gga gtg ttg ttg aac ttt gag gac gtt aac ggg aaa gtg tgg agg				780
Lys Gly Val Leu Leu Asn Phe Glu Asp Val Asn Gly Lys Val Trp Arg	225	230	235	
ttc cgt tac tcg tat tgg aac agt agt cag agt tat gtt ttg act aaa				828
Phe Arg Tyr Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val Leu Thr Lys	240	245	250	255
ggg tgg agc agg ttc gtt aag gag aag aat cta cgt gct ggt gac gtg				876
Gly Trp Ser Arg Phe Val Lys Glu Lys Asn Leu Arg Ala Gly Asp Val	260	265	270	
gtt agt ttc agt aga tct aac ggt cag gat caa cag ttg tac att ggg				924
Val Ser Phe Ser Arg Ser Asn Gly Gln Asp Gln Gln Leu Tyr Ile Gly	275	280	285	
tgg aag tcg aga tcc ggg tca gat tta gat gcg ggt cgg gtt ttg aga				972
Trp Lys Ser Arg Ser Gly Ser Asp Leu Asp Ala Gly Arg Val Leu Arg	290	295	300	
ttg ttc gga gtt aac att tca ccg gag agt tca aga aac gac gtc gta				1020

MBI0018 Sequence Listing.ST25

Leu Phe Gly Val Asn Ile Ser Pro Glu Ser Ser Arg Asn Asp Val Val
 305 310 315
 gga aac aaa aga gtg aac gat act gag atg tta tcg ttg gtg tgt agc 1068
 Gly Asn Lys Arg Val Asn Asp Thr Glu Met Leu Ser Leu Val Cys Ser
 320 325 330 335
 aag aag caa cgc atc ttt cac gcc tcg taa caactcttct tctttttttt 1118
 Lys Lys Gln Arg Ile Phe His Ala Ser
 340
 tcttttgttg ttttaataat ttttaaaaac tccatttttcg ttttctttat ttgcatcggc 1178
 tcttttcttc ttgtttacca aaggttcatg agttgttttt gttgtattga tgaactgtaa 1238
 attttattta taggataaat ttttaaaaaa aaaaaaaaaa aaa 1281

 <210> 36
 <211> 344
 <212> PRT
 <213> Arabidopsis thaliana

 <400> 36
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 1 5 10 15
 Cys Glu Thr Pro Ala Ile Thr Pro Ala Lys Lys Ser Ser Val Gly Asn
 20 25 30
 Leu Tyr Arg Met Gly Ser Gly Ser Ser Val Val Leu Asp Ser Glu Asn
 35 40 45
 Gly Val Glu Ala Glu Ser Arg Lys Leu Pro Ser Ser Lys Tyr Lys Gly
 50 55 60
 Val Val Pro Gln Pro Asn Gly Arg Trp Gly Ala Gln Ile Tyr Glu Lys
 65 70 75 80
 His Gln Arg Val Trp Leu Gly Thr Phe Asn Glu Glu Asp Glu Ala Ala
 85 90 95
 Arg Ala Tyr Asp Val Ala Val His Arg Phe Arg Arg Arg Asp Ala Val
 100 105 110
 Thr Asn Phe Lys Asp Val Lys Met Asp Glu Asp Glu Val Asp Phe Leu
 115 120 125
 Asn Ser His Ser Lys Ser Glu Ile Val Asp Met Leu Arg Lys His Thr
 130 135 140
 Tyr Asn Glu Glu Leu Glu Gln Ser Lys Arg Arg Arg Asn Gly Asn Gly
 145 150 155 160
 Asn Met Thr Arg Thr Leu Leu Thr Ser Gly Leu Ser Asn Asp Gly Val
 165 170 175
 Ser Thr Thr Gly Phe Arg Ser Ala Glu Ala Leu Phe Glu Lys Ala Val
 180 185 190
 Thr Pro Ser Asp Val Gly Lys Leu Asn Arg Leu Val Ile Pro Lys His
 195 200 205

MBI0018 Sequence Listing.ST25

His Ala Glu Lys His Phe Pro Leu Pro Ser Ser Asn Val Ser Val Lys
210 215 220

Gly Val Leu Leu Asn Phe Glu Asp Val Asn Gly Lys Val Trp Arg Phe
225 230 235 240

Arg Tyr Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val Leu Thr Lys Gly
245 250 255

Trp Ser Arg Phe Val Lys Glu Lys Asn Leu Arg Ala Gly Asp Val Val
260 265 270

Ser Phe Ser Arg Ser Asn Gly Gln Asp Gln Gln Leu Tyr Ile Gly Trp
275 280 285

Lys Ser Arg Ser Gly Ser Asp Leu Asp Ala Gly Arg Val Leu Arg Leu
290 295 300

Phe Gly Val Asn Ile Ser Pro Glu Ser Ser Arg Asn Asp Val Val Gly
305 310 315 320

Asn Lys Arg Val Asn Asp Thr Glu Met Leu Ser Leu Val Cys Ser Lys
325 330 335

Lys Gln Arg Ile Phe His Ala Ser
340

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<212> DNA
<213> Arabidopsis thaliana

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<222> (76)..(1077)
<223> G1930

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atctcgtttc ataac atg gat gcc atg agt agc gta gac gag agc tct aca 111
Met Asp Ala Met Ser Ser Val Asp Glu Ser Ser Thr
1 5 10
act aca gat tcc att ccg gcg aga aag tca tcg tct ccg gcg agt tta 159
Thr Thr Asp Ser Ile Pro Ala Arg Lys Ser Ser Ser Pro Ala Ser Leu
15 20 25
cta tat aga atg gga agc gga aca agc gtg gta ctt gat tca gag aac 207
Leu Tyr Arg Met Gly Ser Gly Thr Ser Val Val Leu Asp Ser Glu Asn
30 35 40
ggt gtc gaa gtc gaa gtc gaa gcc gaa tca aga aag ctt cct tct tca 255
Gly Val Glu Val Glu Val Glu Ala Glu Ser Arg Lys Leu Pro Ser Ser
45 50 55 60
aga ttc aaa ggt gtt gtt cct caa cca aat gga aga tgg gga gct cag 303
Arg Phe Lys Gly Val Val Pro Gln Pro Asn Gly Arg Trp Gly Ala Gln
65 70 75
att tac gag aaa cat caa cgc gtg tgg ctt ggt act ttc aac gag gaa 351
Ile Tyr Glu Lys His Gln Arg Val Trp Leu Gly Thr Phe Asn Glu Glu
80 85 90

MBI0018 Sequence Listing.ST25

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gac gaa gca gct cgt gct tac gac gtc gcg gct cac cgt ttc cgt ggc      399
Asp Glu Ala Ala Arg Ala Tyr Asp Val Ala Ala His Arg Phe Arg Gly
      95                      100                      105

cgc gat gcc gtt act aat ttc aaa gac acg acg ttc gaa gaa gag gtt      447
Arg Asp Ala Val Thr Asn Phe Lys Asp Thr Thr Phe Glu Glu Glu Val
      110                      115                      120

gag ttc tta aac gcg cat tcg aaa tca gag atc gta gat atg ttg aga      495
Glu Phe Leu Asn Ala His Ser Lys Ser Glu Ile Val Asp Met Leu Arg
      125                      130                      135

aaa cac act tac aaa gaa gag tta gac caa agg aaa cgt aac cgt gac      543
Lys His Thr Tyr Lys Glu Glu Leu Asp Gln Arg Lys Arg Asn Arg Asp
      145                      150                      155

ggg aac gga aaa gag acg acg gcg ttt gct ttg gct tcg atg ttg gtt      591
Gly Asn Gly Lys Glu Thr Thr Ala Phe Ala Leu Ala Ser Met Val Val
      160                      165                      170

atg acg ggg ttt aaa acg gcg gag tta ctg ttt gag aaa acg gta acg      639
Met Thr Gly Phe Lys Thr Ala Glu Leu Leu Phe Glu Lys Thr Val Thr
      175                      180                      185

cca agt gac gtc ggg aaa cta aac cgt tta gtt ata cca aaa cac caa      687
Pro Ser Asp Val Gly Lys Leu Asn Arg Leu Val Ile Pro Lys His Gln
      190                      195                      200

gcg gag aaa cat ttt ccg tta ccg tta ggt aat aat aac gtc tcc gtt      735
Ala Glu Lys His Phe Pro Leu Pro Leu Gly Asn Asn Asn Val Ser Val
      205                      210                      215

aaa ggt atg ctg ttg aat ttc gaa gac gtt aac ggg aaa gtg tgg agg      783
Lys Gly Met Leu Leu Asn Phe Glu Asp Val Asn Gly Lys Val Trp Arg
      225                      230                      235

ttc cgt tac tct tat tgg aat agt agt caa agt tat gtg ttg acc aaa      831
Phe Arg Tyr Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val Leu Thr Lys
      240                      245                      250

ggg tgg agt aga ttc gtt aaa gag aag aga ctt tgt gct ggt gat ttg      879
Gly Trp Ser Arg Phe Val Lys Glu Lys Arg Leu Cys Ala Gly Asp Leu
      255                      260                      265

atc agt ttt aaa aga tcc aac gat caa gat caa aaa ttc ttt atc ggg      927
Ile Ser Phe Lys Arg Ser Asn Asp Gln Asp Gln Phe Phe Ile Gly
      270                      275                      280

tgg aaa tcg aaa tcc ggg ttg gat cta gag acg ggt cgg gtt atg aga      975
Trp Lys Ser Lys Ser Gly Leu Asp Leu Glu Thr Gly Arg Val Met Arg
      285                      290                      295

ttg ttt ggg gtt gat att tct tta aac gcc gtc gtt gta gtg aag gaa      1023
Leu Phe Gly Val Asp Ile Ser Leu Asn Ala Val Val Val Val Lys Glu
      305                      310                      315

aca acg gag gtg tta atg tcg tcg tta agg tgt aag aag caa cga gtt      1071
Thr Thr Glu Val Leu Met Ser Ser Leu Arg Cys Lys Lys Gln Arg Val
      320                      325                      330

ttg taa taacaattta acaacttggg aaagaaaaaa aagctttttg attttaattt      1127
Leu

ctcttcaacg ttaatcttgc tgagatta      1155

<210> 38
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<212> PRT
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<400> 38

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MBI0018 Sequence Listing.ST25

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Gly Ser Gly Thr Ser Val Val Leu Asp Ser Glu Asn Gly Val Glu Val
 35 40 45

Glu Val Glu Ala Glu Ser Arg Lys Leu Pro Ser Ser Arg Phe Lys Gly
 50 55 60

Val Val Pro Gln Pro Asn Gly Arg Trp Gly Ala Gln Ile Tyr Glu Lys
 65 70 75 80

His Gln Arg Val Trp Leu Gly Thr Phe Asn Glu Glu Asp Glu Ala Ala
 85 90 95

Arg Ala Tyr Asp Val Ala Ala His Arg Phe Arg Gly Arg Asp Ala Val
 100 105 110

Thr Asn Phe Lys Asp Thr Thr Phe Glu Glu Glu Val Glu Phe Leu Asn
 115 120 125

Ala His Ser Lys Ser Glu Ile Val Asp Met Leu Arg Lys His Thr Tyr
 130 135 140

Lys Glu Glu Leu Asp Gln Arg Lys Arg Asn Arg Asp Gly Asn Gly Lys
 145 150 155 160

Glu Thr Thr Ala Phe Ala Leu Ala Ser Met Val Val Met Thr Gly Phe
 165 170 175

Lys Thr Ala Glu Leu Leu Phe Glu Lys Thr Val Thr Pro Ser Asp Val
 180 185 190

Gly Lys Leu Asn Arg Leu Val Ile Pro Lys His Gln Ala Glu Lys His
 195 200 205

Phe Pro Leu Pro Leu Gly Asn Asn Asn Val Ser Val Lys Gly Met Leu
 210 215 220

Leu Asn Phe Glu Asp Val Asn Gly Lys Val Trp Arg Phe Arg Tyr Ser
 225 230 235 240

Tyr Trp Asn Ser Ser Gln Ser Tyr Val Leu Thr Lys Gly Trp Ser Arg
 245 250 255

Phe Val Lys Glu Lys Arg Leu Cys Ala Gly Asp Leu Ile Ser Phe Lys
 260 265 270

Arg Ser Asn Asp Gln Asp Gln Lys Phe Phe Ile Gly Trp Lys Ser Lys
 275 280 285

Ser Gly Leu Asp Leu Glu Thr Gly Arg Val Met Arg Leu Phe Gly Val
 290 295 300

MBI0018 Sequence Listing.ST25

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Leu Met Ser Ser Leu Arg Cys Lys Lys Gln Arg Val Leu
325 330

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<222> (1)..(1035)
<223> G1594

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1 5 10 15
atg atg tca ccg gag agt ctc atg ttt cct tcc gat tac caa gct ttg 96
Met Met Ser Pro Glu Ser Leu Met Phe Pro Ser Asp Tyr Gln Ala Leu
20 25 30
cta tgt tcc tcc gcc ggt gaa aat cgt gtc tct gat gtt ttc gga tcc 144
Leu Cys Ser Ser Ala Gly Glu Asn Arg Val Ser Asp Val Phe Gly Ser
35 40 45
gac gag cta ctc tca gta gcc gtc tcc gct ttg tcg tcg gag gcg gct 192
Asp Glu Leu Leu Ser Val Ala Val Ser Ala Leu Ser Ser Glu Ala Ala
50 55 60
tcg atc gct ccg gag atc cga aga aat gat gat aac gtt tct cta act 240
Ser Ile Ala Pro Glu Ile Arg Arg Asn Asp Asp Asn Val Ser Leu Thr
65 70 75 80
gtc atc aaa gct aaa atc gct tgt cat cct tcg tat cct cgc tta ctt 288
Val Ile Lys Ala Lys Ile Ala Cys His Pro Ser Tyr Pro Arg Leu Leu
85 90 95
caa gct tac atc gat tgc caa aag gtc gga gca cca ccg gag ata gcg 336
Gln Ala Tyr Ile Asp Cys Gln Lys Val Gly Ala Pro Pro Glu Ile Ala
100 105 110
tgt tta cta gag gag att caa cgg gag agt gat gtt tat aag caa gag 384
Cys Leu Leu Glu Glu Ile Gln Arg Glu Ser Asp Val Tyr Lys Gln Glu
115 120 125
gtt gtt cct tct tct tgc ttt gga gct gat cct gag ctt gat gaa ttt 432
Val Val Pro Ser Ser Cys Phe Gly Ala Asp Pro Glu Leu Asp Glu Phe
130 135 140
atg gaa acg tac tgc gat ata tta gtg aaa tac aaa tcg gat cta gca 480
Met Glu Thr Tyr Cys Asp Ile Leu Val Lys Tyr Lys Ser Asp Leu Ala
145 150 155 160
aga ccg ttt gac gag gca acg tgt ttc ttg aac aag att gag atg cag 528
Arg Pro Phe Asp Glu Ala Thr Cys Phe Leu Asn Lys Ile Glu Met Gln
165 170 175
cta cgg aac cta tgt act ggt gtc gag tct gcc agg gga gtt tct ggg 576
Leu Arg Asn Leu Cys Thr Gly Val Glu Ser Ala Arg Gly Val Ser Gly
180 185 190
ggg atg tct cct cat ggg gac aag act att agt cct ctc ctg aca aat 624
Gly Met Ser Pro His Gly Asp Lys Thr Ile Ser Pro Leu Leu Thr Asn
195 200 205
gac aat gga gag gat ggt gta ata tca tct gac gag gaa ctg agt gga 672
Asp Asn Gly Glu Asp Gly Val Ile Ser Ser Asp Glu Glu Leu Ser Gly

MBI0018 Sequence Listing.ST25

210	215	220	
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gac ctc aaa gat agg ttg cta cgc aaa ttt gga agc cgt att agt act Asp Leu Lys Asp Arg Leu Leu Arg Lys Phe Gly Ser Arg Ile Ser Thr 245 250 255			768
tta aag ctt gag ttc tca aag aag aag aag aaa gga aag tta cca aga Leu Lys Leu Glu Phe Ser Lys Lys Lys Lys Gly Lys Leu Pro Arg 260 265 270			816
gaa gca aga caa gct ctt ctt gat tgg tgg aat ctc cat tat aag tgg Glu Ala Arg Gln Ala Leu Leu Asp Trp Trp Asn Leu His Tyr Lys Trp 275 280 285			864
cct tac cct act gaa gga gat aag ata gca tta gct gat gca acg ggg Pro Tyr Pro Thr Glu Gly Asp Lys Ile Ala Leu Ala Asp Ala Thr Gly 290 295 300			912
tta gac caa aaa caa atc aac aat tgg ttt ata aac caa agg aaa cgt Leu Asp Gln Lys Gln Ile Asn Asn Trp Phe Ile Asn Gln Arg Lys Arg 305 310 315 320			960
cat tgg aag cca tca gag aat atg cct ttc gct atg atg gat gat tct His Trp Lys Pro Ser Glu Asn Met Pro Phe Ala Met Met Asp Asp Ser 325 330 335			1008
agt gga tca ttc ttt acc gag gaa tga Ser Gly Ser Phe Phe Thr Glu Glu 340			1035

<210> 40
 <211> 344
 <212> PRT
 <213> Arabidopsis thaliana

<400> 40

Met Tyr Asn Phe His Ser Ala Gly Asp Tyr Ser Asp Lys Ser Val Leu
 1 5 10 15

Met Met Ser Pro Glu Ser Leu Met Phe Pro Ser Asp Tyr Gln Ala Leu
 20 25 30

Leu Cys Ser Ser Ala Gly Glu Asn Arg Val Ser Asp Val Phe Gly Ser
 35 40 45

Asp Glu Leu Leu Ser Val Ala Val Ser Ala Leu Ser Ser Glu Ala Ala
 50 55 60

Ser Ile Ala Pro Glu Ile Arg Arg Asn Asp Asp Asn Val Ser Leu Thr
 65 70 75 80

Val Ile Lys Ala Lys Ile Ala Cys His Pro Ser Tyr Pro Arg Leu Leu
 85 90 95

Gln Ala Tyr Ile Asp Cys Gln Lys Val Gly Ala Pro Pro Glu Ile Ala
 100 105 110

Cys Leu Leu Glu Glu Ile Gln Arg Glu Ser Asp Val Tyr Lys Gln Glu
 115 120 125

Val Val Pro Ser Ser Cys Phe Gly Ala Asp Pro Glu Leu Asp Glu Phe

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130
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 140
 Met Glu Thr Tyr Cys Asp Ile Leu Val Lys Tyr Lys Ser Asp Leu Ala
 145 150 155 160
 Arg Pro Phe Asp Glu Ala Thr Cys Phe Leu Asn Lys Ile Glu Met Gln
 165 170 175
 Leu Arg Asn Leu Cys Thr Gly Val Glu Ser Ala Arg Gly Val Ser Gly
 180 185 190
 Gly Met Ser Pro His Gly Asp Lys Thr Ile Ser Pro Leu Leu Thr Asn
 195 200 205
 Asp Asn Gly Glu Asp Gly Val Ile Ser Ser Asp Glu Glu Leu Ser Gly
 210 215 220
 Gly Asp His Glu Val Ala Glu Asp Gly Arg Gln Arg Cys Glu Asp Arg
 225 230 235 240
 Asp Leu Lys Asp Arg Leu Leu Arg Lys Phe Gly Ser Arg Ile Ser Thr
 245 250 255
 Leu Lys Leu Glu Phe Ser Lys Lys Lys Lys Lys Gly Lys Leu Pro Arg
 260 265 270
 Glu Ala Arg Gln Ala Leu Leu Asp Trp Trp Asn Leu His Tyr Lys Trp
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 Pro Tyr Pro Thr Glu Gly Asp Lys Ile Ala Leu Ala Asp Ala Thr Gly
 290 295 300
 Leu Asp Gln Lys Gln Ile Asn Asn Trp Phe Ile Asn Gln Arg Lys Arg
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 Pro Asp Lys Gly Leu Asp Ser Gly Lys Tyr Val Arg Tyr Thr Pro Glu
 20 25 30

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tct cta aga aga caa caa ctc ata cgt gaa tgt ccg att ctc tct aac Ser Leu Arg Arg Gln Gln Ile Arg Glu Cys Pro Ile Leu Ser Asn 50 55 60	192
atc gag cct aag cag atc aaa gtt tgg ttt cag aac cgc aga tgt cgt Ile Glu Pro Lys Gln Ile Lys Val Trp Phe Gln Asn Arg Arg Cys Arg 65 70 75 80	240
gag aag cag agg aaa gaa gct gct cgt ctt caa aca gtg aac aga aaa Glu Lys Gln Arg Lys Glu Ala Ala Arg Leu Gln Thr Val Asn Arg Lys 85 90 95	288
ctc aat gcc atg aac aaa ctc ttg atg gaa gag aat gat cgt ttg cag Leu Asn Ala Met Asn Lys Leu Leu Met Glu Glu Asn Asp Arg Leu Gln 100 105 110	336
aag caa gtt tct aac ttg gtc tat gag aat ggc cac atg aaa cat caa Lys Gln Val Ser Asn Leu Val Tyr Glu Asn Gly His Met Lys His Gln 115 120 125	384
ctt cac act gct tct ggg acg acc aca gac aac agc tgt gag tct gtg Leu His Thr Ala Ser Gly Thr Thr Asp Asn Ser Cys Glu Ser Val 130 135 140	432
gtc gtg agt ggt cag caa cat caa cag caa aac cca aat cct cag cat Val Val Ser Gly Gln Gln His Gln Gln Gln Asn Pro Asn Pro Gln His 145 150 155 160	480
cag caa cgt gat gct aac aac cca gca gga ctc ctt tct ata gca gag Gln Gln Arg Asp Ala Asn Asn Pro Ala Gly Leu Leu Ser Ile Ala Glu 165 170 175	528
gag gcc cta gca gag ttc ctt tcc aag gct aca gga act gct gtt gac Glu Ala Leu Ala Phe Leu Ser Lys Ala Thr Gly Thr Ala Val Asp 180 185 190	576
tgg gtt cag atg att ggg atg aag cct ggt ccg gat tct att ggc ata Trp Val Gln Met Ile Gly Met Lys Pro Gly Pro Asp Ser Ile Gly Ile 195 200 205	624
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ctc gtg agt tta gaa ccc atg aag gtt gct gaa att ctc aaa gat cgt Leu Val Ser Leu Glu Pro Met Lys Val Ala Glu Ile Leu Lys Asp Arg 225 230 235 240	720
cca tct tgg ctc cga gat tgt cga agt gtg gat act ctg agt gtg ata Pro Ser Trp Leu Arg Asp Cys Arg Ser Val Asp Thr Leu Ser Val Ile 245 250 255	768
cct gct gga aac ggt ggg acg atc gag ctt att tac acg cag atg tat Pro Ala Gly Asn Gly Gly Thr Ile Glu Leu Ile Tyr Thr Gln Met Tyr 260 265 270	816
gct cct acg act tta gca gca gct cgt gac ttt tgg acg ctg aga tat Ala Pro Thr Thr Leu Ala Ala Ala Arg Asp Phe Trp Thr Leu Arg Tyr 275 280 285	864
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act tct gca act ggt ggc ccc act ggg cca cct tct tca aac ttt gtg Thr Ser Ala Thr Gly Gly Pro Thr Gly Pro Pro Ser Ser Asn Phe Val 305 310 315 320	960
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ggt ggt tcc att ctc cac att gtt gat cat gtt gat ctg gat gcc tgg Gly Gly Ser Ile Leu His Ile Val Asp His Val Asp Leu Asp Ala Trp 340 345 350	1056
agt gtc cct gaa gtc atg agg cct ctc tat gaa tca tcg aag att ctt Ser Val Pro Glu Val Met Arg Pro Leu Tyr Glu Ser Ser Lys Ile Leu 355 360 365	1104
gct cag aaa atg act gtt gct gct ttg aga cat gta aga caa att gca Ala Gln Lys Met Thr Val Ala Ala Leu Arg His Val Arg Gln Ile Ala 370 375 380	1152
caa gaa aca agt gga gaa gtt cag tat ggt gga ggg cgc caa cct gcg Gln Glu Thr Ser Gly Glu Val Gln Tyr Gly Gly Arg Gln Pro Ala 385 390 400	1200
gtt tta aga acc ttc agt caa aga ctc tgt cgg ggt ttc aat gat gct Val Leu Arg Thr Phe Ser Gln Arg Leu Cys Arg Gly Phe Asn Asp Ala 405 410 415	1248
gtt aat ggt ttt gtg gat gat gga tgg tca cca atg ggt agc gat ggt Val Asn Gly Phe Val Asp Asp Gly Trp Ser Pro Met Gly Ser Asp Gly 420 425 430	1296
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ggg tct cag tac ggt aat tca ttc ctt cca agc ttt ggt agt ggc gtg Gly Ser Gln Tyr Gly Asn Phe Leu Pro Ser Phe Gly Ser Gly Val 450 455 460	1392
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ctg gtt cga ttc ctt aga gaa cac cga tct gaa tgg gct gat tat ggc Leu Val Arg Phe Leu Arg Glu His Arg Ser Glu Trp Ala Asp Tyr Gly 485 490 495	1488
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gaa ggt cac gct tac tca ccc gaa gac atg ggt tta gct cgg gat atg Glu Gly His Ala Tyr Ser Pro Glu Asp Met Gly Leu Ala Arg Asp Met 545 550 555 560	1680
tat ttg cta cag ctt tgt agc ggt gtt gat gaa aat gtg gtt gga ggt Tyr Leu Leu Gln Leu Cys Ser Gly Val Asp Glu Asn Val Val Gly Gly 565 570 575	1728
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gca cct ttg ctt cct tcc ggt ttc cgc atc ata cct ctt gaa cag aaa Ala Pro Leu Leu Pro Ser Gly Phe Arg Ile Ile Pro Leu Glu Gln Lys 595 600 605	1824
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Asn His Ser Arg Asp Ser Val Ala Ser Met Ala Arg Gln Tyr Val Arg				
	660	665	670	
agc ata gta gga tcg att cag agg gtt gct cta gcc att gct cct cgt				2064
Ser Ile Val Gly Ser Ile Gln Arg Val Ala Leu Ala Ile Ala Pro Arg				
	675	680	685	
cct ggc tcc aat atc agt cca ata tct gtt ccc act tcc cct gaa gct				2112
Pro Gly Ser Asn Ile Ser Pro Ile Ser Val Pro Thr Ser Pro Glu Ala				
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ctc act ctg gtc cgt tgg atc tcc cgg agt tac agc ctt cac act ggt				2160
Leu Thr Leu Val Arg Trp Ile Ser Arg Ser Tyr Ser Leu His Thr Gly				
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Ala Asp Leu Phe Gly Ser Asp Ser Gln Thr Ser Gly Asp Thr Leu Leu				
	725	730	735	
cat caa ctc tgg aat cac tct gat gca atc ttg tgc tgc tcc ctc aaa				2256
His Gln Leu Trp Asn His Ser Asp Ala Ile Leu Cys Cys Ser Leu Lys				
	740	745	750	
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Thr				
ggaaacgact cttgtagccc ttcaagacat aatgctagac aagacccttg acgaacctgg				2369
tcgtaaagct ctttgcctcg agttcccca gatcatgcaa cagggtatg ctcatctgcc				2429
ggcaggagta tgtgcgtcaa gcatgggaag gatggtatct tacgagcagg caacggtgtg				2489
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Ser Leu Arg Arg Gln Gln Leu Ile Arg Glu Cys Pro Ile Leu Ser Asn				
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Ile Glu Pro Lys Gln Ile Lys Val Trp Phe Gln Asn Arg Arg Cys Arg				
	65	70	75	80
Glu Lys Gln Arg Lys Glu Ala Ala Arg Leu Gln Thr Val Asn Arg Lys				
	85	90	95	

MBI0018 Sequence Listing.ST25

Leu Asn Ala Met Asn Lys Leu Leu Met Glu Glu Asn Asp Arg Leu Gln
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 Lys Gln Val Ser Asn Leu Val Tyr Glu Asn Gly His Met Lys His Gln
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 Leu His Thr Ala Ser Gly Thr Thr Thr Asp Asn Ser Cys Glu Ser Val
 130 135 140
 Val Val Ser Gly Gln Gln His Gln Gln Gln Asn Pro Asn Pro Gln His
 145 150 155 160
 Gln Gln Arg Asp Ala Asn Asn Pro Ala Gly Leu Leu Ser Ile Ala Glu
 165 170 175
 Glu Ala Leu Ala Glu Phe Leu Ser Lys Ala Thr Gly Thr Ala Val Asp
 180 185 190
 Trp Val Gln Met Ile Gly Met Lys Pro Gly Pro Asp Ser Ile Gly Ile
 195 200 205
 Val Ala Ile Ser Arg Asn Cys Ser Gly Ile Ala Ala Arg Ala Cys Gly
 210 215 220
 Leu Val Ser Leu Glu Pro Met Lys Val Ala Glu Ile Leu Lys Asp Arg
 225 230 235 240
 Pro Ser Trp Leu Arg Asp Cys Arg Ser Val Asp Thr Leu Ser Val Ile
 245 250 255
 Pro Ala Gly Asn Gly Gly Thr Ile Glu Leu Ile Tyr Thr Gln Met Tyr
 260 265 270
 Ala Pro Thr Thr Leu Ala Ala Ala Arg Asp Phe Trp Thr Leu Arg Tyr
 275 280 285
 Ser Thr Cys Leu Glu Asp Gly Ser Tyr Val Val Cys Glu Arg Ser Leu
 290 295 300
 Thr Ser Ala Thr Gly Gly Pro Thr Gly Pro Pro Ser Ser Asn Phe Val
 305 310 315 320
 Arg Ala Glu Met Lys Pro Ser Gly Phe Leu Ile Arg Pro Cys Asp Gly
 325 330 335
 Gly Gly Ser Ile Leu His Ile Val Asp His Val Asp Leu Asp Ala Trp
 340 345 350
 Ser Val Pro Glu Val Met Arg Pro Leu Tyr Glu Ser Ser Lys Ile Leu
 355 360 365
 Ala Gln Lys Met Thr Val Ala Ala Leu Arg His Val Arg Gln Ile Ala
 370 375 380
 Gln Glu Thr Ser Gly Glu Val Gln Tyr Gly Gly Gly Arg Gln Pro Ala
 385 390 395 400

MBI0018 Sequence Listing.ST25

Val Leu Arg Thr Phe Ser Gln Arg Leu Cys Arg Gly Phe Asn Asp Ala
 405 410 415

Val Asn Gly Phe Val Asp Asp Gly Trp Ser Pro Met Gly Ser Asp Gly
 420 425 430

Ala Glu Asp Val Thr Val Met Ile Asn Leu Ser Pro Gly Lys Phe Gly
 435 440 445

Gly Ser Gln Tyr Gly Asn Ser Phe Leu Pro Ser Phe Gly Ser Gly Val
 450 455 460

Leu Cys Ala Lys Ala Ser Met Leu Leu Gln Asn Val Pro Pro Ala Val
 465 470 475 480

Leu Val Arg Phe Leu Arg Glu His Arg Ser Glu Trp Ala Asp Tyr Gly
 485 490 495

Val Asp Ala Tyr Ala Ala Ala Ser Leu Arg Ala Ser Pro Phe Ala Val
 500 505 510

Pro Cys Ala Arg Ala Gly Gly Phe Pro Ser Asn Gln Val Ile Leu Pro
 515 520 525

Leu Ala Gln Thr Val Glu His Glu Glu Ser Leu Glu Val Val Arg Leu
 530 535 540

Glu Gly His Ala Tyr Ser Pro Glu Asp Met Gly Leu Ala Arg Asp Met
 545 550 555 560

Tyr Leu Leu Gln Leu Cys Ser Gly Val Asp Glu Asn Val Val Gly Gly
 565 570 575

Cys Ala Gln Leu Val Phe Ala Pro Ile Asp Glu Ser Phe Ala Asp Asp
 580 585 590

Ala Pro Leu Leu Pro Ser Gly Phe Arg Ile Ile Pro Leu Glu Gln Lys
 595 600 605

Ser Thr Pro Asn Gly Ala Ser Ala Asn Arg Thr Leu Asp Leu Ala Ser
 610 615 620

Ala Leu Glu Gly Ser Thr Arg Gln Ala Gly Glu Ala Asp Pro Asn Gly
 625 630 635 640

Cys Asn Phe Arg Ser Val Leu Thr Ile Ala Phe Gln Phe Thr Phe Asp
 645 650 655

Asn His Ser Arg Asp Ser Val Ala Ser Met Ala Arg Gln Tyr Val Arg
 660 665 670

Ser Ile Val Gly Ser Ile Gln Arg Val Ala Leu Ala Ile Ala Pro Arg
 675 680 685

Pro Gly Ser Asn Ile Ser Pro Ile Ser Val Pro Thr Ser Pro Glu Ala

MBI0018 Sequence Listing.ST25

690 695 700

Leu Thr Leu Val Arg Trp Ile Ser Arg Ser Tyr Ser Leu His Thr Gly
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Ala Asp Leu Phe Gly Ser Asp Ser Gln Thr Ser Gly Asp Thr Leu Leu
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Phe Asp Ser Gly Lys Tyr Val Arg Tyr Thr Pro Glu Gln Val Glu Ala	
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Leu Glu Arg Val Tyr Ala Glu Cys Pro Lys Pro Ser Ser Leu Arg Arg	
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Gln Gln Leu Ile Arg Glu Cys Pro Ile Leu Cys Asn Ile Glu Pro Arg	
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Gln Ile Lys Val Trp Phe Gln Asn Arg Arg Cys Arg Glu Lys Gln Arg	
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Lys Glu Ser Ala Arg Leu Gln Thr Val Asn Arg Lys Leu Ser Ala Met	
85 90 95	
aac aag ctt ttg atg gaa gag aat gat cgt ttg cag aag caa gtc tcc	336
Asn Lys Leu Leu Met Glu Glu Asn Asp Arg Leu Gln Lys Gln Val Ser	
100 105 110	
aac ttg gtt tat gag aat gga ttc atg aaa cat cga atc cac act gct	384
Asn Leu Val Tyr Glu Asn Gly Phe Met Lys His Arg Ile His Thr Ala	
115 120 125	
tct ggg acg acc aca gac aac agc tgt gag tct gtg gtc gtg agt ggt	432
Ser Gly Thr Thr Thr Asp Asn Ser Cys Glu Ser Val Val Val Ser Gly	
130 135 140	
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Gln Gln Arg Gln Gln Asn Pro Thr His Gln His Pro Gln Arg Asp	
145 150 155 160	
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Val Asn Asn Pro Ala Asn Leu Leu Ser Ile Ala Glu Glu Thr Leu Ala	
165 170 175	

MBI0018 Sequence Listing.ST25

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att ggg atg aag cct ggt ccg gat tct att ggt atc gta gct gtt tca Ile Gly Met Lys Pro Gly Pro Asp Ser Ile Gly Ile Val Ala Val Ser 195 200 205	624
cgc aac tgc agt gga ata gca gca cgt gcc tgt ggc ctc gtg agt tta Arg Asn Cys Ser Gly Ile Ala Ala Arg Ala Cys Gly Leu Val Ser Leu 210 215 220	672
gaa ccc atg aag gtc gct gaa atc ctc aaa gat cgt cca tct tgg ttc Glu Pro Met Lys Val Ala Glu Ile Leu Lys Asp Arg Pro Ser Trp Phe 225 230 235 240	720
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gct tct atg ctg ttg cag aat gtt cca ccc ctt gta ttg att cgg ttc Ala Ser Met Leu Leu Gln Asn Val Pro Pro Leu Val Leu Ile Arg Phe 465 470 475 480	1440

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ctc gaa cat gaa gag ttt ctc gaa gtg gtt aga ctt gga ggt cat gct Leu Glu His Glu Glu Phe Leu Glu Val Val Arg Leu Gly Gly His Ala 530 535 540	1632
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cct tct ggt ttc cgt gtc ata cca ctc gac caa aaa aca aat ccg aat Pro Ser Gly Phe Arg Val Ile Pro Leu Asp Gln Lys Thr Asn Pro Asn 595 600 605	1824
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aca atg gcg aga cag tat gtg agg aac gtt gtt ggt tcg att cag aga Thr Met Ala Arg Gln Tyr Val Arg Asn Val Val Gly Ser Ile Gln Arg 660 665 670	2016
gtg gct cta gcc att acg cct cgt cct ggc tca atg caa ctt ccc act Val Ala Leu Ala Ile Thr Pro Arg Pro Gly Ser Met Gln Leu Pro Thr 675 680 685	2064
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Ser Glu Phe Ala Lys Ile Met Gln Gln Gly Tyr Ala Asn Leu Pro Ala
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MBI0018 Sequence Listing.ST25

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MBI0018 Sequence Listing.ST25

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MBI0018 Sequence Listing.ST25

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MBI0018 Sequence Listing.ST25

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 660 665 670

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WO 01/36444

PCT/US00/31325

MBI0018 Sequence Listing.ST25
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Trp Ser Phe Val
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INTERNATIONAL SEARCH REPORT

national application No.

PC/T/US00/31325

A. CLASSIFICATION OF SUBJECT MATTER

IPC(7) : C07H 21/04; C12N 5/10, 15/29, 15/63, 15/82
US Cl. : 435/320.1, 419, 440, 468; 536/23.1, 23.6; 800/278, 290

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 435/320.1, 419, 440, 468; 536/23.1, 23.6; 800/278, 290

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
Please See Continuation Sheet

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	Database Genbank on NCBI, US National Library of Medicine (Bethesda, MD, USA). No. AJ005196, BUCHHOLZ, G. et al. 'Nuclear-localized receiver-like proteins are differentially expressed in Arabidopsis thaliana'. September 4, 1998.	4,6,9,10
Y	SAKAI, H. et al. Two-component response regulators from Arabidopsis thaliana contain a putative DNA-binding motif. Plant Cell Physiology 1998, Vol 39 No. 11, pages 1232-1239, see entire document.	1-3,5,7,8,9,13,27-27
X	GLOVER, B.J. et al. Development of several epidermal cell types can be specified by the same MYB-related plant transcription factor. Development 1998, Vol 125, pages 3497-3508, see entire document.	4,6
Y	MARTIN, C. et al. MYB transcription factors in plants. Trends in Genetics, February 1997, Vol 13, No 2, pages 67-73, see entire document.	1-10, 13, 25-27
A		1-10, 13, 25-27

☐ Further documents are listed in the continuation of Box C.

☐ See patent family annex.

Special categories of cited documents:	
"A" document defining the general state of the art which is not considered to be of particular relevance	"I" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"E" earlier application or patent published on or after the international filing date	"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"I" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"O" document referring to an oral disclosure, use, exhibition or other means	"R" document member of the same patent family
"P" document published prior to the international filing date but later than the priority date claimed	

Date of the actual completion of the international search

04 April 2001 (04.04.2001)

Date of publication of the international search report

03 MAY 2001

Name and mailing address of the ISA/US

Commissioner of Patents and Trademarks

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INTERNATIONAL SEARCH REPORT

International application No.

PCT/US00/31325

Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claim Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claim Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☒ Claim Nos.: 14 and 23
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:
Please See Continuation Sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☒ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.: 1-10, 13, 25-27 and SEQ ID NO: 1, 2, 29 & 30.
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest



The additional search fees were accompanied by the applicant's protest.

No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US00/31325

BOX II. OBSERVATIONS WHERE UNITY OF INVENTION IS LACKING This application contains the following inventions or groups of inventions which are not so linked as to form a single general inventive concept under PCT Rule 13.1. In order for all inventions to be examined, the appropriate additional examination fees must be paid.

This application contains the following inventions or groups of inventions which are not so linked as to form a single general inventive concept under PCT Rule 13.1. In order for all inventions to be examined, the appropriate additional examination fees must be paid.

Groups I-XXIII, claim(s) 1-10, 13, 14 and 25-27, drawn to a transgenic plant having modified structure and development characteristics, polynucleotides and vectors for producing said transgenic plant and a method of making said transgenic plant. Applicant must elect one pair of sequences (one nucleic acid and the corresponding amino acid translation) to be examined, *i.e.* SEQ ID NO: 1 and 2 in Group I, SEQ ID NO: 3 and 4 in Group II, SEQ ID NO: 5 and 6 in Group III, etc.

Group XXIV, claim(s) 11 and 12, drawn to an isolated or recombinant polypeptide.

Group XXV, claim(s) 15-17, drawn to a method of identifying a factor that is modulated by or interacts with a polypeptide.

Group XXVI, claim(s) 18, drawn to a method of identifying a molecule that modulates activity or expression of a polynucleotide or polypeptide.

Group XXVII, claim(s) 19 and 20, drawn to an integrated data system.

Group XXVIII, claim(s) 21-24, drawn to a method of identifying a polynucleotide or polypeptide sequence homologue.

The inventions listed as Groups I-XXVIII do not relate to a single general inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons:

The inventions listed as Groups I-XXVIII do not relate to a single general inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons: Groups I-XXIII are drawn to a transgenic plant and a method of producing said plant with a nucleic acid sequence encoding a wide variety of transcription factors. Group XXIV is drawn to a wide variety of isolated or recombinant polypeptides having transcriptional factor activity. The methods of Groups I-XXIII differ from each other in that they are directed to a plant transformation method and transgenic plant with a structurally and functionally distinct nucleic acid sequence which encodes a structurally and functionally distinct amino acid sequence. In addition, Groups XXV, XXVI, XXVII and XXVIII are different methods from any of Groups I-XXIII in that they have different method steps and different end products, and Group XXVII requires a computer system. Thus, there is no single special technical feature, which links the inventions of Groups I-XXVIII under PCT Rule 13.2.

Continuation of B. FIELDS SEARCHED Item 3: EAST (USPAT); STN (AGRICOLA, BIOSIS, CAPLUS, EMBASE); Sequence Search SEQ ID NO: 1, 2, 29 and 30; NCBI/Genbank.

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